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W A P E S R L A  
(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.  
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MPSrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm  
Run on: Sun Sep 13 07:26:01 1998; MasPar time 4580.90 Seconds  
Tabular output not generated. 1340.595 Million cell updates/sec

Title: >US-08-554-424-7  
Description: (1-6513) from US08554424.seq  
Perfect Score: 6513  
N.A. Sequence: 1 TCTAGACGTTGGCGCATAG.....ACGCGAGTATTAGCTCTAGA 6513  
Comp: AGATCTGCAACCGCGTATC.....TGGCTCATATCGAGATCT

Scoring table: TABLE default  
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 1460335 seqs, 471452172 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: n-pending  
1:P9 2:U6000 3:U6001 4:U6002 5:U6003 6:U6004 7:U6005  
8:U6006 9:U6007 10:U6008 11:U7 12:U80 13:U81 14:U82  
15:U83 16:U84A 17:U84B 18:U85 19:U86 20:U87 21:U88  
22:U89 23:U90A 24:U90B 25:U91 26:NEWP 27:NEWU8 28:NEWU9

Statistics: Mean 11.841; Variance 4.073; scale 2.907

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	6513	100.0	6513	18	US-08-554- Sequence 7, Applicatio	0.00e+00
2	5500	84.4	6519	21	US-08-808- Sequence 24, Applicati	0.00e+00
3	4374	67.2	5461	11	US-07-998- Sequence 7, Applicatio	0.00e+00
4	4374	67.2	5461	11	US-07-998- Sequence 7, Applicatio	0.00e+00
5	3676	56.4	6318	21	US-08-808- Sequence 1, Applicatio	0.00e+00
6	3676	56.4	6318	20	US-08-772- Sequence 1, Applicatio	0.00e+00
7	3676	56.4	6318	1	US-08-772- Sequence 2, Applicatio	0.00e+00
8	3664	56.3	6315	20	US-08-808- Sequence 2, Applicatio	0.00e+00
9	3664	56.3	6315	21	US-08-808- Sequence 2, Applicatio	0.00e+00
10	3664	56.3	6315	20	US-08-808- Sequence 2, Applicatio	0.00e+00
11	3662	56.2	6318	19	US-08-608- Sequence 1, Applicatio	0.00e+00
12	3660	56.2	6318	19	US-08-608- Sequence 2, Applicatio	0.00e+00
13	472	7.2	1237	21	US-08-808- Sequence 26, Applicati	0.00e+00
14	356	5.5	5977	23	US-09-024- Sequence 1, Applicatio	0.00e+00
15	356	5.5	6007	23	US-09-024- Sequence 2, Applicatio	0.00e+00
16	356	5.5	6556	23	US-09-024- Sequence 7, Applicatio	0.00e+00
17	354	5.4	6826	23	US-09-024- Sequence 8, Applicatio	0.00e+00

18	320	4.9	6048	19	US-08-682- Sequence 1, Applicatio	0.00e+00
19	316	4.9	6452	21	US-08-836- Sequence 9, Applicatio	0.00e+00
20	312	4.8	3033	15	US-08-334- Sequence 1, Applicatio	0.00e+00
21	312	4.8	3033	21	US-08-836- Sequence 1, Applicatio	0.00e+00
22	308	4.7	6371	21	US-08-836- Sequence 13, Applicati	0.00e+00
23	308	4.7	6404	21	US-08-836- Sequence 14, Applicati	0.00e+00
24	298	4.6	6344	18	US-08-511- Sequence 1, Applicatio	0.00e+00
25	298	4.6	6344	21	US-08-843- Sequence 1, Applicatio	0.00e+00
26	296	4.5	6524	20	US-08-775- Sequence 1, Applicatio	0.00e+00
27	296	4.5	6524	19	US-08-669- Sequence 1, Applicatio	0.00e+00
28	296	4.5	6527	19	US-08-669- Sequence 7, Applicatio	0.00e+00
29	296	4.5	6527	20	US-08-775- Sequence 7, Applicatio	0.00e+00
30	296	4.5	7052	20	US-08-775- Sequence 5, Applicatio	0.00e+00
31	296	4.5	7052	19	US-08-669- Sequence 5, Applicatio	0.00e+00
32	254	3.9	5874	21	US-08-843- Sequence 9, Applicatio	1.28e-256
33	231	3.5	2573	19	US-08-669- Sequence 3, Applicatio	5.85e-229
34	231	3.5	2573	20	US-08-775- Sequence 3, Applicatio	5.85e-229
35	214	3.3	930	19	US-08-605- Sequence 2, Applicatio	1.32e-208
36	204	3.1	930	19	US-08-605- Sequence 21, Applicati	1.12e-196
37	194	3.0	930	19	US-08-605- Sequence 3, Applicatio	8.85e-185
38	192	2.9	930	19	US-08-605- Sequence 1, Applicatio	2.10e-182
39	177	2.7	2279	11	US-07-998- Sequence 3, Applicatio	1.20e-164
40	177	2.7	2279	11	US-07-998- Sequence 3, Applicatio	1.20e-164
41	171	2.6	696	23	US-08-024- Sequence 5, Applicatio	1.43e-157
42	148	2.3	5482	15	US-08-346- Sequence 2, Applicatio	1.26e-130
43	134	2.1	702	18	US-08-511- Sequence 3, Applicatio	2.16e-114
44	134	2.1	702	21	US-08-843- Sequence 3, Applicatio	2.16e-114
45	119	1.8	5389	15	US-08-346- Sequence 1, Applicatio	3.57e-97

ALIGNMENTS

RESULT 1  
ID US-08-554-424-7 STANDARD; DNA; UNC; 6513 BP.  
AC xxxxxx

DE Sequence 7, Application US/08554424  
CC Sequence 7, Application US/08554424  
CC GENERAL INFORMATION:  
CC APPLICANT: Warmke, Jeffrey W.  
CC APPLICANT: Van Der Ploeg, Leonardus

CC TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE  
CC TITLE OF INVENTION: PARA SODIUM CHANNEL  
CC NUMBER OF SEQUENCES: 7  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Jack L. Tribble  
CC STREET: P.O. Box 2000, 125 E. Lincoln Avenue  
CC CITY: Rahway  
CC STATE: New Jersey  
CC COUNTRY: USA  
CC ZIP: 07065-0907

CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: PatentIn Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/554,424  
CC FILING DATE:  
CC CLASSIFICATION: 424  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Tribble, Jack L.  
CC REGISTRATION NUMBER: 32,633  
CC REFERENCE/DOCKET NUMBER: 19338DA

CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (908) 594-5321  
CC TELEFAX: (908) 594-4720  
CC INFORMATION FOR SEQ ID NO: 7:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 6513 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear

mind

CC MOLECULE TYPE: cDNA  
SQ SEQUENCE 6513 BP; 1681 A; 1548 C; 1702 G; 1582 T; 0 OTHER.

Query Match 100.0%; Score 6513; DB 18; Length 6513;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 TCTAGACGTTGGCCGATAGACAATGACAGAAGATTCGACATCGATATCTGAGGAAGAAC 60  
Qy 1 TCTAGACGTTGGCCGATAGACAATGACAGAAGATTCGACATCGATATCTGAGGAAGAAC 60  
Db 61 GCAGTTTGTTCGTCCTTACCCGGAATCATTTGGTCAAAATCGAACAACGATTCGCG 120  
Qy 61 GCAGTTTGTTCGTCCTTACCCGGAATCATTTGGTCAAAATCGAACAACGATTCGCG 120  
Db 121 CTGAACATGAAAGCAGAGGAGCTGGAAAGAAAGAGCCGAGGAGAGGTGCCCGCAT 180  
Qy 121 CTGAACATGAAAGCAGAGGAGCTGGAAAGAAAGAGCCGAGGAGAGGTGCCCGCAT 180  
Db 181 ATGGTCGCAAGAAAACAAAAGAAATCCGATATGATGACGAGGACGAGGATGAAGTC 240  
Qy 181 ATGGTCGCAAGAAAACAAAAGAAATCCGATATGATGACGAGGACGAGGATGAAGTC 240  
Db 241 CACACCGGATCCTACACTTGAACAGGGTGTGCCAATACCTTTCGATTGCAGGCGACT 300  
Qy 241 CACACCGGATCCTACACTTGAACAGGGTGTGCCAATACCTTTCGATTGCAGGCGACT 300  
Db 301 TCCCGCGGAATGGCCCTCCACTCTCGAGGATATCGATCCCTTACAGCAATGTAC 360  
Qy 301 TCCCGCGGAATGGCCCTCCACTCTCGAGGATATCGATCCCTTACAGCAATGTAC 360  
Db 361 TGACATTCGTAGTTGAACAAAGAAAGATATTTTCGCTTTTCGTGATCAAAAGCAA 420  
Qy 361 TGACATTCGTAGTTGAACAAAGAAAGATATTTTCGCTTTTCGTGATCAAAAGCAA 420  
Db 421 TGTGGATGTCGATCAATCAATCCGATACGTCGTCGGCCATTTACATTCAGTGCATC 480  
Qy 421 TGTGGATGTCGATCAATCAATCCGATACGTCGTCGGCCATTTACATTCAGTGCATC 480  
Db 481 CATTAATTTCCCTATTCATCATCACCAATTCCTCAACTGCATCGCATGATAATGC 540  
Qy 481 CATTAATTTCCCTATTCATCATCACCAATTCCTCAACTGCATCGCATGATAATGC 540  
Db 541 CGAACAGCCCGGTTGAGTCCACTGAGGTGATATTCACCGGAATCTACACATTTGAAT 600  
Qy 541 CGAACAGCCCGGTTGAGTCCACTGAGGTGATATTCACCGGAATCTACACATTTGAAT 600  
Db 601 CAGCTGTTAAAGTGTGGCAGCAGGTTTCATTTTATGCCGTTTACGTATCTTAGAGTG 660  
Qy 601 CAGCTGTTAAAGTGTGGCAGCAGGTTTCATTTTATGCCGTTTACGTATCTTAGAGTG 660  
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Qy 661 CATGGAATGGCTGGACTTCGTAGTAATAGCTTTAGCTTTATGTGACCATGGGTATAGATT 720  
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Qy 721 TAGGTAATCTAGAGCCCTGCGAACCTTTTAGGTGCTGCGAGCGTTAAACCGTAGCCA 780  
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Qy 781 TTGTGCGAGGCTGAAGACCATCGTCGGCGCGTCATCGAATCGGTGAAGAACTCTCGCG 840  
Db 841 ATGTGATTAATCTGACCATGTTCTCCCTGTCGGGTTCGCGTTGATGGCCCTACAGATCT 900  
Qy 841 ATGTGATTAATCTGACCATGTTCTCCCTGTCGGGTTCGCGTTGATGGCCCTACAGATCT 900  
Db 901 ATATGGGCTGCTACCCGAGAGTGCATCAAGAAGTTCCCGTGGAGCGGTTCCCTGGGGCA 960  
Qy 901 ATATGGGCTGCTACCCGAGAGTGCATCAAGAAGTTCCCGTGGAGCGGTTCCCTGGGGCA 960  
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Qy 961 ATCTGACCGACGAGACTGGGACTATCAATCGCAATAGCTCCCAATTTGTTCCGAGG 1020

Qy 961 ATCTGACCGACGAGAACTGGGACTATACAAATCCCAATAGTCCCAATTTGGTATTCGAGG 1020  
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Qy 1021 ACGAGGCACTCTCATTTCCGTTATGCGGCAATATATCCGTCGGGGCAATGCGACGACG 1080  
Db 1081 ATTACGTTGCTCGACGGGTTTGGTCCGAATCCGAATTTATGCTACACAGCTTCGATT 1140  
Qy 1081 ATTACGTTGCTCGACGGGTTTGGTCCGAATCCGAATTTATGCTACACAGCTTCGATT 1140  
Db 1141 CGTTCCGATGGCTTCTCTGTCGCCCTTCCGGCTGATGACACAGGACTTCTGGGAGATC 1200  
Qy 1141 CGTTCCGATGGCTTCTCTGTCGCCCTTCCGGCTGATGACACAGGACTTCTGGGAGATC 1200  
Db 1201 TGTACCACTGCTGTTTGGCGCCCGGACCATGGCACATGCTGCTTTTATAGTCATCA 1260  
Qy 1201 TGTACCACTGCTGTTTGGCGCCCGGACCATGGCACATGCTGCTTTTATAGTCATCA 1260  
Db 1261 TCTTCTTAGTTCAATTCATCTTGTGAATTTGATTTGGCCATTTGTTGCCATGTCGTATG 1320  
Qy 1261 TCTTCTTAGTTCAATTCATCTTGTGAATTTGATTTGGCCATTTGTTGCCATGTCGTATG 1320  
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Qy 1321 ACGAATTGCAAGGAAGGCGGAAAGAGAGGCTGCCGAAGAGAGGCGGATAGCTGAAG 1380  
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Qy 1381 CGGAAGAGCTGCCGCCGCCCAAGCGGCTGGAGGAGCGGCCAATGCGCAGGCTC 1440  
Db 1441 AGGCAGACGCGGATGGGCTGCCGCCCGAAGAGGCTGCATCGCATCCGGAATGCCAAGA 1500  
Qy 1441 AGGCAGACGCGGATGGGCTGCCGCCCGAAGAGGCTGCATCGCATCCGGAATGCCAAGA 1500  
Db 1501 GTCCGACATCTTCTGATCAGCTATGAGCTATTTTGGCGCGAGAAGGCGCAACGATG 1560  
Qy 1501 GTCCGACATCTTCTGATCAGCTATGAGCTATTTTGGCGCGAGAAGGCGCAACGATG 1560  
Db 1561 ACAACAACAAAGAGAAGATGTCCATTCGGAGCTGCGAGTGGAGTCCGAGTTCGAGCG 1620  
Qy 1561 ACAACAACAAAGAGAAGATGTCCATTCGGAGCTGCGAGTGGAGTTCGAGTTCGAGCG 1620  
Db 1621 TTATACAAGACACAGCAGCCTACCAGACACACCAAGCTACCAGTTCGTAAGTGA 1680  
Qy 1621 TTATACAAGACACAGCAGCCTACCAGACACACCAAGCTACCAGTTCGTAAGTGA 1680  
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Qy 1681 GCAGACATCTTATCTTACCTGTTTACCGTTTAAACATACGCGGGGATCAGCTAGTT 1740  
Db 1741 CTCACAAGTACACGATACGGAACGAGCTGGCCGCTTTGGTATACCCGGTAGCGATCGTA 1800  
Qy 1741 CTCACAAGTACACGATACGGAACGAGCTGGCCGCTTTGGTATACCCGGTAGCGATCGTA 1800  
Db 1801 AGCCATTTGGTATTTGTAACATATCAGGATGCCAGCAGCTTCCCTATGCCAGCAGCT 1860  
Qy 1801 AGCCATTTGGTATTTGTAACATATCAGGATGCCAGCAGCTTCCCTATGCCAGCAGCT 1860  
Db 1861 CGAATGCCCTCACCCCGATGTCGGAAGAGATGGGCCATCATAGTCCCGTGTACTATG 1920  
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Db 1921 GCAATCTAGGCTCCCGACACTCATCTATACCTCGCATCAGTCCCGAATATCGTATACCT 1980  
Qy 1921 GCAATCTAGGCTCCCGACACTCATCTATACCTCGCATCAGTCCCGAATATCGTATACCT 1980  
Db 1981 CATATGGCGATCTACTCGCGCGCATGGCCGTCATGGGGGTGAGCACAATGACCAAGAGA 2040  
Qy 1981 CATATGGCGATCTACTCGCGCGCATGGCCGTCATGGGGGTGAGCACAATGACCAAGAGA 2040  
Db 2041 GCAAAATTCGCAACCGCAACACACGCAATCAATCAGTGGGCGCCCAATGGCGCACCA 2100  
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Db 2101 CCTGCTGACACCAATACAAAGCTCGATCATCGGACTACGAAATTGGCCTGGAGTGA 2160  
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Db 2101 CCTGCTGGACACCAATACAAAGCTCGATCATCGGACTACGAAATTGGCCTGGAGTGA 2160  
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Db 2161 CGGACGAAGCTGGCAAGATTAAACATCATGACAATCTCTTTATCGAGCCGCTCCAGACAC 2220  
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Db 2221 AAACGGTGGTGTGATGAAAGATGTGATGCTCCTGAATGACATCATCGAACAGCCGCTG 2280  
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Db 2281 GTCCGACAGTGGGCAAGCATCGCGGTGCTCGGTTTACTATTCCCAACAGAGGAG 2340  
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Db 2401 ATGTGTTTTGTGTGGGACTGTGTGGGTTTGGTTGAAATTCAGGAGTGGGTATCGC 2460  
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Db 3181 CCGATAACGATACGATAAAATAGCCGAGGCGCTTCAATCGAATTTGGCCGATTTAAAAGTT 3240  
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Db 3481 TACACGGGACATGAAGAACCAACAGCCGAAGAAATCCAAATATCTAAATACGCAACGA 3540  
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Db 3601 GTTTCCTCTTACAGGACGACGACTCCAGCATTAATCAATATGTTAGTGGTATAGATC 3660  
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Db 3661 GACCAATTAAGGACGAGAGCCACAGGCGCAGACGATGGAGCGCGGAGGAGGAGGAGC 3720  
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Db 3841 AATATCCAGCTGATTCCTCCCGGATTCGTACTATAAGAAATTTCCGATCTTAGCCGGTG 3900  
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Db 3841 AATATCCAGCTGATTCCTCCCGGATTCGTACTATAAGAAATTTCCGATCTTAGCCGGTG 3900  
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Db 3901 ACGATGACTCGCGCTTCTGGCAAGGATGGGCAATTTACGACTGAAACTTTTCAATTA 3960  
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Db 3901 ACGATGACTCGCGCTTCTGGCAAGGATGGGCAATTTACGACTGAAACTTTTCAATTA 3960  
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Db 3961 TTGAAAATAAATATTTTGAACAGCTGTATCATCTATGATTTAATGAGTAGCTTAGCTT 4020  
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Db 3961 TTGAAAATAAATATTTTGAACAGCTGTATCATCTATGATTTAATGAGTAGCTTAGCTT 4020  
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Db 4021 TGGCAATTAAGAGATGATCATCTGCGCAAAAGACCCATCTGCGAGGATATTTTATATA 4080  
QY |||||  
Db 4021 TGGCAATTAAGAGATGATCATCTGCGCAAAAGACCCATCTGCGAGGATATTTTATATA 4080  
QY |||||  
Db 4081 TGGACAGAATATTTACGGTTATTTCTTCTTGGAAATGTTAATCAAGTGGTTGGCGCTCG 4140  
QY |||||  
Db 4081 TGGACAGAATATTTACGGTTATTTCTTCTTGGAAATGTTAATCAAGTGGTTGGCGCTCG 4140  
QY |||||  
Db 4141 GCTTCAAGTGTACTTACCAACGCGTGTGGCTCGATTCGATTCGATTCGATTCGATTC 4200  
QY |||||  
Db 4141 GCTTCAAGTGTACTTACCAACGCGTGTGGCTCGATTCGATTCGATTCGATTCGATTC 4200  
QY |||||  
Db 4201 CGCTTATCAACTTCGTTGCTTCACTTGTGGAGCTGGTATTCAGGCTTCAAGACTA 4260  
QY |||||  
Db 4201 CGCTTATCAACTTCGTTGCTTCACTTGTGGAGCTGGTATTCAGGCTTCAAGACTA 4260  
QY |||||  
Db 4261 TCGCAACGTTAAGAGCACTGAGACCACTACGTGCCATGTCCCGTATGCGAGGCGATGAGG 4320

|||||  
4261 TGGAAAGCTTAAGAGCACTGAGACCCTAGCTGCGCATGTCCGCTATGCAAGGCATGAGGG 4320  
Db  
4321 TCGTCGTTAATCGCTGGTACAGCATATACGGTCCATCTTCATGTGCTATTGGTGTGC 4380  
Qy  
4321 TCGTCGTTAATCGCTGGTACAGCATATACGGTCCATCTTCATGTGCTATTGGTGTGC 4380  
Db  
4381 TAATATTTTGGCTAAATTTTGGCCATAATGGGTGTACAGCTTTTTCGTGGAAATATTTTA 4440  
Qy  
4381 TAATATTTTGGCTAAATTTTGGCCATAATGGGTGTACAGCTTTTTCGTGGAAATATTTTA 4440  
Db  
4441 AGTCGAGGACATGAATGGCAGCAAGCTCAGCCACGAGATCATACCAAAATCGCAATGCC 4500  
Qy  
4441 AGTCGAGGACATGAATGGCAGCAAGCTCAGCCACGAGATCATACCAAAATCGCAATGCC 4500  
Db  
4501 GCGAGCGGAGAACTACAGCTGGGTGAATTCAGCAATGAATTCGATCATGTAGGTAACG 4560  
Qy  
4501 GCGAGCGGAGAACTACAGCTGGGTGAATTCAGCAATGAATTCGATCATGTAGGTAACG 4560  
Db  
4561 CGTATCTGTGCTTTTCCAAAGTGCCACCTTCAAAGGCTGGATACAAATCATGAACGATG 4620  
Qy  
4561 CGTATCTGTGCTTTTCCAAAGTGCCACCTTCAAAGGCTGGATACAAATCATGAACGATG 4620  
Db  
4621 CTATCGATTACGAGAGGTGGACAAAGCAACCAATTCGTGAACAAATCATGATGATT 4680  
Qy  
4621 CTATCGATTACGAGAGGTGGACAAAGCAACCAATTCGTGAACAAATCATGATGATT 4680  
Db  
4681 TATATTTGCTATCTTCATCATATTTTGGATCTTTTTCACACTCAATCTGTTCAATGGTG 4740  
Qy  
4681 TATATTTGCTATCTTCATCATATTTTGGATCTTTTTCACACTCAATCTGTTCAATGGTG 4740  
Db  
4741 TTATCATTTGATAATTTTAAATGAGCAAAAGAAAAGCAGGTGGATCATTAGAAATGTTCA 4800  
Qy  
4741 TTATCATTTGATAATTTTAAATGAGCAAAAGAAAAGCAGGTGGATCATTAGAAATGTTCA 4800  
Db  
4801 TGACAGAGATCAGAAAAGTACTATATGCTATGAAAGAGATGGGCTCTAAAAACCAT 4860  
Qy  
4801 TGACAGAGATCAGAAAAGTACTATATGCTATGAAAGAGATGGGCTCTAAAAACCAT 4860  
Db  
4861 TAAAGCCATTCCAAAGACCAAGGTGGGACCAAGCAATAGTCTTGAATAGTAACCG 4920  
Qy  
4861 TAAAGCCATTCCAAAGACCAAGGTGGGACCAAGCAATAGTCTTGAATAGTAACCG 4920  
Db  
4921 ATAGAAATTCGATATATCATTATGTTATTTATTTGCTGAACATGTTCAACCATGACC 4980  
Qy  
4921 ATAGAAATTCGATATATCATTATGTTATTTATTTGCTGAACATGTTCAACCATGACC 4980  
Db  
4981 TCGATCGTTACGATCGCTCGGACACGATATACGGCGTCTTAGACTATCTCAATCGGATAT 5040  
Qy  
4981 TCGATCGTTACGATCGCTCGGACACGATATACGGCGTCTTAGACTATCTCAATCGGATAT 5040  
Db  
5041 TCGTAGTTATTTTTCAGTTCCGAATGCTCTATTAAAAATATTCGCTTTACGATATCATTAT 5100  
Qy  
5041 TCGTAGTTATTTTTCAGTTCCGAATGCTCTATTAAAAATATTCGCTTTACGATATCATTAT 5100  
Db  
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Qy  
5101 TTATTAGCCATGGAATTTATTTGATGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG 5160  
Db  
5161 TACTTAGCGATATATCAGAAAGTACTTCTGCTGCGGACCCCTGCTCCGAGTGGTGGTG 5220  
Qy  
5161 TACTTAGCGATATATCAGAAAGTACTTCTGCTGCGGACCCCTGCTCCGAGTGGTGGTG 5220  
Db  
5221 TGGCAAAAGTGGGCGTCTCTTCGACTGGTGAAGGGAGCCAAAGGCAATTCGGACACTGC 5280  
Qy  
5221 TGGCAAAAGTGGGCGTCTCTTCGACTGGTGAAGGGAGCCAAAGGCAATTCGGACACTGC 5280  
Db  
5281 TCTTCGCGTTGGCCATGTCGCTGGCGGCCCTGTTCAACATCTGCTGCTGCTGCTGCTGCTG 5340  
Qy  
5281 TCTTCGCGTTGGCCATGTCGCTGGCGGCCCTGTTCAACATCTGCTGCTGCTGCTGCTGCTG 5340  
Db  
5341 TCATGTTTCATCTTTCGCAATTTTCGCAATGCTGCTTTCATGCAAGTGAAGGAGAGCG 5400  
|||||

Qy 5341 TCATGTTTCATCTTTGCCATTTTTCGCAATGCTGCTTCTTCATGCAAGGAGAGAGCG 5400  
Db 5401 GCATTAACGACGCTTACAACTTTCAAGACCTTTGGCCAGAGCATGATCTGCTCTTTTCA 5460  
Qy 5401 GCATTAACGACGCTTACAACTTTCAAGACCTTTGGCCAGAGCATGATCTGCTCTTTTCA 5460  
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Qy 5461 TGTGACGCTCAGCCGTTGGGATGTTGCTGAGCGCCATTATCAATGAGGAAGCATGCG 5520  
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Qy 5521 ATCCACCCGACAGCAGCAAAAGGCTATCGGGCAATTTGTTTCAGCGACCTTTGGAATAA 5580  
Db 5581 CGTTTCTCCTCTCATACCTAGTTAAGCTTTTAAAGCTTTTGTATAGTTTAAATATGATGCTG 5640  
Qy 5581 CGTTTCTCCTCTCATACCTAGTTAAGCTTTTAAAGCTTTTGTATAGTTTAAATATGATGCTG 5640  
Db 5641 TCATTTCTGAGAACTATAGTCAGGCCACCGAGGAGCTGCAAGAGGCTCTAACCGACGCG 5700  
Qy 5641 TCATTTCTGAGAACTATAGTCAGGCCACCGAGGAGCTGCAAGAGGCTCTAACCGACGCG 5700  
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Qy 5701 ACTACGACATGTACTATGAGATCTGGCAGCAATTCGATCCGGAGGCAACCCAGTACATAC 5760  
Db 5761 GCTATGATCAGCTGTCCGAAATTCCTGAGCTACTGAGGCCGCCGCTGCAAGATCCCAAA 5820  
Qy 5761 GCTATGATCAGCTGTCCGAAATTCCTGAGCTACTGAGGCCGCCGCTGCAAGATCCCAAA 5820  
Db 5821 CGAAAGTACAAGATCATATCGATGGACATACCCATCTGTCGCGGTGACCTCATGTACT 5880  
Qy 5821 CGAAAGTACAAGATCATATCGATGGACATACCCATCTGTCGCGGTGACCTCATGTACT 5880  
Db 5881 GCGTCAACATCTCTGAGCGCCCTTACGAAAGACTCTTTTCGCGGGAAGGCAATCCGATAG 5940  
Qy 5881 GCGTCAACATCTCTGAGCGCCCTTACGAAAGACTCTTTTCGCGGGAAGGCAATCCGATAG 5940  
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Qy 5941 AGGAGACGGGTGAGATTGTTGATAGATACGCGCCGCCGCGATACGGAGGCTACGAGCCCG 6000  
Db 6001 TCTCATCAACGCTGTGGCGTACGCGTACGAGTACTGCGCCGCGTAAATCCAGCAGCCT 6060  
Qy 6001 TCTCATCAACGCTGTGGCGTACGCGTACGAGTACTGCGCCGCGTAAATCCAGCAGCCT 6060  
Db 6061 GCGAAAGCACAGCGCGCGGAGGAGTGGGTCTTTGAGCCGCGATACGGATCATG 6120  
Qy 6061 GCGAAAGCACAGCGCGCGGAGGAGTGGGTCTTTGAGCCGCGATACGGATCATG 6120  
Db 6121 GCGATGCGGTGATCCGGATGCGCGGACCCGCGCCGCGATGAAGCAACGAGCGCGATG 6180  
Qy 6121 GCGATGCGGTGATCCGGATGCGCGGACCCGCGCCGCGATGAAGCAACGAGCGCGATG 6180  
Db 6181 CGCCCGTGTGAGATGTTAGTGTAAAGCTACTGCAAGAGGAGTGGCGATGCGCGATG 6240  
Qy 6181 CGCCCGTGTGAGATGTTAGTGTAAAGCTACTGCAAGAGGAGTGGCGATGCGCGATG 6240  
Db 6241 AGAGTAAATGTAATAGTCCGGGTGAGGATGCAAGGAGGAGTGGGTCTTTGAGCCGCGATACGGATCATG 6300  
Qy 6241 AGAGTAAATGTAATAGTCCGGGTGAGGATGCAAGGAGGAGTGGGTCTTTGAGCCGCGATACGGATCATG 6300  
Db 6301 CGCGCGCGCGGACGACGACGCGGAGTCCCGGAGCGGCTAGCGCGCGCGGACGAGCAG 6360  
Qy 6301 CGCGCGCGCGGACGACGACGCGGAGTCCCGGAGCGGCTAGCGCGCGCGGACGAGCAG 6360  
Db 6361 CGCGCGTTCGTGAGAGCGCGGTTGTTAGCAAGAAACGCGCCACAGAGTGGTGTATCC 6420  
Qy 6361 CGCGCGTTCGTGAGAGCGCGGTTGTTAGCAAGAAACGCGCCACAGAGTGGTGTATCC 6420  
Db 6421 ACTCGGATCGCGAGCATCAGCTCGCGACGCGGATGTTCTGAGCAGGCGCTCGCCCC 6480  
Qy 6421 ACTCGGATCGCGAGCATCAGCTCGCGACGCGGATGTTCTGAGCAGGCGCTCGCCCC 6480



Db 6481 CCTCAAGATGACCGGAGTATTAGTCTAGA 6513  
QY 6481 CCTCAAGATGACCGGAGTATTAGTCTAGA 6513

RESULT 2  
ID US-08-808-793-24 STANDARD; DNA; UNC; 6519 BP.  
AC xxxxxx

DT Sequence 24, Application US/08808793  
DE Sequence 24, Application US/08808793  
CC GENERAL INFORMATION:  
CC APPLICANT: Soderlund, David M.  
CC APPLICANT: Ingles, Patricia J.  
CC TITLE OF INVENTION: CALCIUM PERMEABLE INSECT SODIUM CHANNELS  
CC TITLE OF INVENTION: AND USE THEREOF  
CC NUMBER OF SEQUENCES: 32  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP  
CC STREET: Clinton Square, P.O. Box 1051  
CC CITY: Rochester  
CC STATE: New York  
CC COUNTRY: USA  
CC ZIP: 14603

CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: PatentIn Release #1.0, Version #1.30  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/808,793  
CC FILING DATE:  
CC CLASSIFICATION: 435  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 60/034,361  
CC FILING DATE: 24-DEC-1996  
CC CLASSIFICATION: 435  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 60/012,649  
CC FILING DATE: 01-MAR-1996  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Braman, Susan J.  
CC REGISTRATION NUMBER: 34,103  
CC REFERENCE/DOCKET NUMBER: 19603/1062 (D-1906A)  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 716-263-1636  
CC TELEFAX: 716-263-1600  
CC INFORMATION FOR SEQ ID NO: 24:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 6519 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: cDNA  
CC SEQUENCE 6519 BP; 1707 A; 1544 C; 1698 G; 1570 T; 0 OTHER.

Query Match 84 48; Score 5500; DB 21; Length 6519;  
Best Local Similarity 97.7; Pred. No. 0.00e+00;  
Matches 6337; Conservative 0; Mismatches 9; Indels 138; Gaps 3;

Db 1 ATGACAGAAGATCCGACTCGATATCTGAGGAAGACGGCAGTTTGTTCGGTCCCTTTACC 60  
QY 24 ATGACAGAAGATCCGACTCGATATCTGAGGAAGACGGCAGTTTGTTCGGTCCCTTTACC 83

Db 61 CGCGAATCATTTGGTGCATAATCGAACACGATTTCCGCTGAACATGAAGAGCAGAAGGAG 120  
QY 84 CGCGAATCATTTGGTGCATAATCGAACACGATTTCCGCTGAACATGAAGAGCAGAAGGAG 143

Db 121 CTGGAAGAAGAGAGCCGAGGAGAGGAGTCCCGCGATATGGTCGCAAGAAAAACAAAAA 180  
QY 144 CTGGAAGAAGAGAGCCGAGGAGAGGAGTCCCGCGATATGGTCGCAAGAAAAACAAAAA 203

Db 181 GAAATCCGATATGATGACGAGGACGAGGATGAAGGTCCACAACCGGATCCTACACTTGA 240  
QY 204 GAAATCCGATATGATGACGAGGACGAGGATGAAGGTCCACAACCGGATCCTACACTTGA 263

Db 241 CAGGGTGTGCCAATACCTGTTCCGATTGACGGGAGCTTCCCGCCGGAATGGGCTCCACT 300  
QY 264 CAGGGTGTGCCAATACCTGTTCCGATTGACGGGAGCTTCCCGCCGGAATGGGCTCCACT 323

Db 301 CCTCTCGAGGATATGATCCCTACTACAGCAATGTACTGACATTCCTAGTGTGTAAGCAAA 360  
QY 324 CCTCTCGAGGATATGATCCCTACTACAGCAATGTACTGACATTCCTAGTGTGTAAGCAAA 383

Db 361 GGAAGAATATTTTTCGCTTTTCTGCAATCAAAAGCAATGTGGATGCTCGATCCATCAAT 420  
QY 384 GGAAGAATATTTTTCGCTTTTCTGCAATCAAAAGCAATGTGGATGCTCGATCCATCAAT 443

Db 421 CGGATACGTCGTGTGGCCATTTACATTTAGTGATCCATTTATTTCCCTATTTCATCATC 480  
QY 444 CGGATACGTCGTGTGGCCATTTACATTTAGTGATCCATTTATTTCCCTATTTCATCATC 503

Db 481 ACCACAATTCGTCAACTGCATCCTGTATGATAATCCGACACGCCACGGTTGAGTCC 540  
QY 504 ACCACAATTCGTCAACTGCATCCTGTATGATAATCCGACACGCCACGGTTGAGTCC 563

Db 541 ACTGAGGTGATATTCACCGGAATCTACACATTTGAATCAGCTGTTAAAGTGATGGCACGA 600  
QY 564 ACTGAGGTGATATTCACCGGAATCTACACATTTGAATCAGCTGTTAAAGTGATGGCACGA 623

Db 601 GGTTCATTTTATGCCCCGTTTACGATATCTTAGAGATGCAATGGAATGGGTGGACTTCGTA 660  
QY 624 GGTTCATTTTATGCCCCGTTTACGATATCTTAGAGATGCAATGGAATGGGTGGACTTCGTA 683

Db 661 GTAATAGCTTTAGCTTATCTGACCATGGGTATAGATTTAGGTAATCTAGCAGCCCTGCGA 720  
QY 684 GTAATAGCTTTAGCTTATCTGACCATGGGTATAGATTTAGGTAATCTAGCAGCCCTGCGA 743

Db 721 AGCTTTAGGGTGTGCGAGCGCTTAAAGCGTAGCCATTTGCGCAGGCTTGAAGACCATC 780  
QY 744 AGCTTTAGGGTGTGCGAGCGCTTAAAGCGTAGCCATTTGCGCAGGCTTGAAGACCATC 803

Db 781 GTCGCGCGCGTCATCGAATCGGTGAAGAACTCTGCGCGATGTGATATCTCGACCATGTTTC 840  
QY 804 GTCGCGCGCGTCATCGAATCGGTGAAGAACTCTGCGCGATGTGATATCTCGACCATGTTTC 863

Db 841 TCCTCTCGGTGTTCGCGTTGATGGCCCTACAGATCTATATGGGCGTGTCCACCGAGAAG 900  
QY 864 TCCTCTCGGTGTTCGCGTTGATGGGCGCTACAGATCTATATGGGCGTGTCCACCGAGAAG 923

Db 901 TGCATCAAGAAGTTCCCGCTGGACGGTTCTTGGGGCAATCTGACCCAGCAGAACTGGGAC 960  
QY 924 TGCATCAAGAAGTTCCCGCTGGACGGTTCTTGGGGCAATCTGACCCAGCAGAACTGGGAC 983

Db 961 TATCACAATCGCAATAGTCCCAATGGTATTCGAGGACGAGGGCATCTCATTTCCGTTA 1020  
QY 984 TATCACAATCGCAATAGTCCCAATGGTATTCGAGGACGAGGGCATCTCATTTCCGTTA 1043

Db 1021 TCGCGCAATATATCCCGTGGGGGCAATCGGACGAGATACGTGTCCCTGCAGGGGTTT 1080  
QY 1044 TCGCGCAATATATCCCGTGGGGGCAATCGGACGAGATACGTGTCCCTGCAGGGGTTT 1103

Db 1081 GGTCCCAATCCGAATTTATGGCTAGACCACTTCTGATTCGTTCCGATGGGCTTTCCTGTCC 1140  
QY 1104 GGTCCCAATCCGAATTTATGGCTAGACCACTTCTGATTCGTTCCGATGGGCTTTCCTGTCC 1163

Db 1141 GCCTTCGGCTGATGACAGGACTTCTGGGAGATCTGTACCAGCTGGTGTGTTCGCGGCC 1200  
QY 1164 GCCTTCGGCTGATGACAGGACTTCTGGGAGATCTGTACCAGCTGGTGTGTTCGCGGCC 1223

Db 1201 GCGGACCATGGACATGCTGTTCTTTATAGTCATCATCTTCTTAGTTCAATTTATCTT 1260  
QY 1224 GCGGACCATGGACATGCTGTTCTTTATAGTCATCATCTTCTTAGTTCAATTTATCTT 1283









QY 2724 GGTGTCCAGGGTGTGTCCTTTCGATTTGCGTTTCCGATTTGCTCGTGTATTCAAACTGGCC 2783  
Db 2698 AGTCTTGCCACACTTAATTTACTTCATTCGATTTATGGAGCAGCACCATGGCGCTTTG 2757  
QY 2784 AGTCTTGCCACACTTAATTTACTTCATTCGATTTATGGAGCAGCACCATGGCGCTTTG 2843  
Db 2758 GGTAACTCTGACATTTGACTTTTGCAATTCATCTTTCGCGTGTATGGGAATGCAA 2817  
QY 2844 GGTAACTCTGACATTTGACTTTTGCAATTCATCTTTCGCGTGTATGGGAATGCAA 2903  
Db 2818 CTGTTGGAAAGAAATTCATGATACACAGGACCGCTTTCCGGATGGCGACCTGGCGGC 2877  
QY 2904 CTGTTGGAAAGAAATTCATGATACACAGGACCGCTTTCCGGATGGCGACCTGGCGGC 2963  
Db 2878 TGGAACTTCACCCACATTTATGACACAGCTTCATGATCGTGTCCGGGTGCTCTCGGAGAA 2937  
QY 2964 TGGAACTTCACCCACATTTATGACACAGCTTCATGATCGTGTCCGGGTGCTCTCGGAGAA 3023  
Db 2938 TGGATCGAGTCCATGTGGGACTGCATGTACGTGGGCGATGTCTCGTGCATTCCTTCCTTC 2997  
QY 3024 TGGATCGAGTCCATGTGGGACTGCATGTACGTGGGCGATGTCTCGTGCATTCCTTCCTTC 3083  
Db 2998 TTGGCCACCGTTGTCATCGGCATCTTGTGGTACTTAACTTTTCTTAGCCTTGTCTTTG 3057  
QY 3084 TTGGCCACCGTTGTCATCGGCATCTTGTGGTACTTAACTTTTCTTAGCCTTGTCTTTG 3143  
Db 3058 TCCAAATTTTGGCTCATCTAGCTTATCAGCGCCGACTGCCGATAAACGATACGAATAAATA 3117  
QY 3144 TCCAAATTTTGGCTCATCTAGCTTATCAGCGCCGACTGCCGATAAACGATACGAATAAATA 3203  
Db 3118 GCGAGGCTTTCATCGAAATTTGCGGANTTTAAAGTTGGGTTAAGCGTAAATTTGCTGAT 3177  
QY 3204 GCGAGGCTTTCATCGAAATTTGCGGANTTTAAAGTTGGGTTAAGCGTAAATTTGCTGAT 3263  
Db 3178 TGTTCAGTTAATACGTAACAATTTGACAAATCAATTAAGTATCAACCCATCAG----- 3232  
QY 3264 TGTTCAGTTAATACGTAACAATTTGACAAATCAATTAAGTATCAACCCATCAGGTGAG 3323  
Db 3233 -----AGCATGGTGACAAACGAACCTGGAGCTG 3258  
QY 3324 AGGACCAACAGATCAGTTGGATTTGGAGCGAAGAGCATGGTGACAACTGGAGCTG 3383  
Db 3259 GGCCACAGCAGATCTTCGCGGACGGCTCATCAAGNAGGGGATCAAGAGCAGAGCGCAA 3318  
QY 3384 GGCCACAGCAGATCTTCGCGGACGGCTCATCAAGNAGGGGATCAAGAGCAGAGCGCAA 3443  
Db 3319 CTGGAGTGGCCATCGGGGATGGCATGGAATTCACGATACACGGCGACATGAAGAACAAC 3378  
QY 3444 CTGGAGTGGCCATCGGGGATCGGATGGAATTCACGATACACGGCGACATGAAGACAAC 3503  
Db 3379 AAGCCGAAGAAATCCAAATATCTTAATAACGCAACG----- 3414  
QY 3504 AAGCCGAAGAAATCCAAATATCTTAATAACGCAACGATATGGCAACTCAATTAACCAAC 3563  
Db 3415 -----GACGCGAC 3423  
QY 3564 CAAGACAATAGACTGGAACACGAGCTAAACCATAGAGGTTTGTCTTACAGGACGAGC 3623  
Db 3424 ACTGCGAGCATTAATCATATGTTAGCCATGAAGAAATCGACCATTCAGAGCAGAGCGCAC 3483  
QY 3624 ACTGCGAGCATTAATCATATGTTAGCCATGAAGAAATCGACCATTCAGAGCAGAGCGCAC 3683  
Db 3484 AAGGCGAGCCGAGACGATGGAGGGGAGAGAGGAGCGGACGCCAGCAGAGGAGATTTA 3543  
QY 3684 AAGGCGAGCCGAGACGATGGAGGGGAGAGAGGAGCGGACGCCAGCAGAGGAGATTTA 3743  
Db 3544 GGTCTCGACGAGGAACCTGACGAGGAGGGGAATGCCAGGAGGCGCGCTCGACGGTGTAT 3603  
QY 3744 GGTCTCGACGAGGAACCTGACGAGGAGGGGAATGCCAGGAGGCGCGCTCGACGGTGTAT 3803  
Db 3604 ATCATTTATTCACACGACGAGGATATCTCGATGAATATCCAGCTGATTTGTCGCCCC 3663  
QY 3804 ATCATTTATTCACACGACGAGGATATCTCGATGAATATCCAGCTGATTTGTCGCCCC 3863

Db 3654 GATTCGTACTATAAGAAATTTCCGATCTTAGCCGGTGACGATGACTCGCGTTCTTGCAA 3723  
QY 3864 GATTCGTACTATAAGAAATTTCCGATCTTAGCCGGTGACGATGACTCGCGTTCTTGCAA 3923  
Db 3724 GGATGGGCAATTTACGACTGAAACCTTTTCGATTAATTTGAGGATAAATTTTGAACA 3783  
QY 3924 GGATGGGCAATTTACGACTGAAACCTTTTCGATTAATTTGAAATAAATTTTGAACA 3983  
Db 3784 GCTGTATCACTATGATTTTAAATGAGTAGCTTAGCTTTGGCATTAGAGATGTACATCTG 3843  
QY 3984 GCTGTATCACTATGATTTTAAATGAGTAGCTTAGCTTTGGCATTAGAGATGTACATCTG 4043  
Db 3844 CCACAAAGACCCATACGACGAGTATTTTATPACTATATGGACAGAAATTTTACGGTTATA 3903  
QY 4044 CCACAAAGACCCATACGACGAGTATTTTATPACTATATGGACAGAAATTTTACGGTTATA 4103  
Db 3904 TTCCTTTGGAAATGTTAAATCAAGTGGTTGGCGCTCGGCTTCAAGTGTACTTGCACCAAC 3963  
QY 4104 TTCCTTTGGAAATGTTAAATCAAGTGGTTGGCGCTCGGCTTCAAGTGTACTTGCACCAAC 4163  
Db 3964 GCGTGGTGTGGCTCGATTTTCGTCATGTCATGTCGCTTATCAACTTCGTTGCTTCA 4023  
QY 4164 GCGTGGTGTGGCTCGATTTTCGTCATGTCATGTCGCTTATCAACTTCGTTGCTTCA 4223  
Db 4024 CTTGTTGGAGCTGGTGGTATTCAGCCCTTCAAGACTATGCGAAGCTTAAAGACACTGAGA 4083  
QY 4224 CTTGTTGGAGCTGGTGGTATTCAGCCCTTCAAGACTATGCGAAGCTTAAAGACACTGAGA 4283  
Db 4084 CCACCTACCTGCGCATGTCCTGATGCAGGGCATGAGGGTGCCTTAATGCCCTGGTCAAA 4143  
QY 4284 CCACCTACCTGCGCATGTCCTGATGCAGGGCATGAGGGTGCCTTAATGCCCTGGTCAAA 4343  
Db 4144 GCTATACCGTCCATCTTCAATGTGCTATTGTTGTCTTAATTTTGGCTAAATTTTGGC 4203  
QY 4344 GCTATACCGTCCATCTTCAATGTGCTATTGTTGTCTTAATTTTGGCTAAATTTTGGC 4303  
Db 4204 ATAATGGTGTACAGCTTTTTCGTTGGAAATATTTTAACTGCGAGGACATGAATGGCAG 4263  
QY 4404 ATAATGGTGTACAGCTTTTTCGTTGGAAATATTTTAACTGCGAGGACATGAATGGCAG 4463  
Db 4264 AAGCTCAGCCAGCAGATCATACCAATCGCAATGCTCGGAGAGCGAAGCTTACACGTGG 4323  
QY 4464 AAGCTCAGCCAGCAGATCATACCAATCGCAATGCTCGGAGAGCGAAGCTTACACGTGG 4523  
Db 4324 GTGAATTCAGCAATGAATTTTCGATCATGTAGTAACGGTATCTGTGCTTTTCCAAGTG 4383  
QY 4524 GTGAATTCAGCAATGAATTTTCGATCATGTAGTAACGGTATCTGTGCTTTTCCAAGTG 4583  
Db 4384 GCCACCTTCAAAGGCTGGATACAAATCATGACGATGCTATCGATTTCAGGAGGTGAC 4443  
QY 4584 GCCACCTTCAAAGGCTGGATACAAATCATGACGATGCTATCGATTTCAGGAGGTGAC 4643  
Db 4444 AAGCAACCAATTCGTTGAAACGAACATCTACATGATTTATATTTTCGTTTCTTCATCATA 4503  
QY 4644 AAGCAACCAATTCGTTGAAACGAACATCTACATGATTTATATTTTCGTTTCTTCATCATA 4703  
Db 4504 TTTGGATCAATTTTTCACACTCAATCTGTTTCATGTTGGTATCATTTGATAAATTTTAAAG 4563  
QY 4704 TTTGGATCAATTTTTCACACTCAATCTGTTTCATGTTGGTATCATTTGATAAATTTTAAAG 4763  
Db 4564 CAAAGAAAAGCAGGTGATCATTAGAAATGTTCAATGACAGAAATGTTCAAGAAAAGTAC 4623  
QY 4764 CAAAGAAAAGCAGGTGATCATTAGAAATGTTCAATGACAGAAATGTTCAAGAAAAGTAC 4823  
Db 4624 TATAGTCTTATGAAAAGATGGGCTCTTAAAAACCATTTAAAAAGCCATTTCCAAAGCAAGG 4683  
QY 4824 TATAGTCTTATGAAAAGATGGGCTCTTAAAAACCATTTAAAAAGCCATTTCCAAAGCAAGG 4883  
Db 4684 TGGCGACACAGCAATAGTCTTTGAAATAGTAACCGGATAAGAAATTCGATATATCATT 4743  
QY 4884 TGGCGACACAGCAATAGTCTTTGAAATAGTAACCGGATAAGAAATTCGATATATCATT 4943





Db 721 ACGTTTAGGGTGTGCGAGCGCTTAAACCGTAGCCATTGTGCCAGGCTTGAAGACATC 780  
Qy |||||  
Db 744 ACGTTTAGGGTGTGCGAGCGCTTAAACCGTAGCCATTGTGCCAGGCTTGAAGACATC 803  
Qy |||||  
Db 781 GTCGGCGCGTCATCGAATCGGTGAAGAACTCTGCGCGATGTGATTATCTCGACCATGTC 840  
Qy |||||  
Db 804 GTCGGCGCGTCATCGAATCGGTGAAGAACTCTGCGCGATGTGATTATCTCGACCATGTC 863  
Qy |||||  
Db 841 TCCCTGTGCGGTGTCGCGCTTGATGGGCTACAGATCTATATGGCGTGTCTCACCGAGAAG 900  
Qy |||||  
Db 864 TCCCTGTGCGGTGTCGCGCTTGATGGGCTACAGATCTATATGGCGTGTCTCACCGAGAAG 923  
Qy |||||  
Db 901 TGCATCAAGAAGTTCCTCGCTCGAGCGTTCCTGGGGCAATCTGACCGAGGAATGGGAC 960  
Qy |||||  
Db 924 TGCATCAAGAAGTTCCTCGCTCGAGCGTTCCTGGGGCAATCTGACCGAGGAATGGGAC 983  
Qy |||||  
Db 961 TATCACAAATCCGAATAGTCCAAATGGTATTCCGAGGACGAGGCGATCTCATTTCCGTTA 1020  
Qy |||||  
Db 984 TATCACAAATCCGAATAGTCCAAATGGTATTCCGAGGACGAGGCGATCTCATTTCCGTTA 1043  
Qy |||||  
Db 1021 TCGGGCAATATATCCGCTGCGGGCAATGCGACGACGATTAACGTGTGCTCGAGGGGTTT 1080  
Qy |||||  
Db 1044 TCGGGCAATATATCCGCTGCGGGCAATGCGACGACGATTAACGTGTGCTCGAGGGGTTT 1103  
Qy |||||  
Db 1081 GGTCCGAATCCGAATATGGCTACACGAGCTTCGATTCTCGGATGGGCTTTCCTGTCC 1140  
Qy |||||  
Db 1104 GGTCCGAATCCGAATATGGCTACACGAGCTTCGATTCTCGGATGGGCTTTCCTGTCC 1163  
Qy |||||  
Db 1141 GCCTTCGCGCTGATGACACAGGACTTCTGGGAGGATCTGTACCAGCTGTGTTCGCGGCC 1200  
Qy |||||  
Db 1164 GCCTTCGCGCTGATGACACAGGACTTCTGGGAGGATCTGTACCAGCTGTGTTCGCGGCC 1223  
Qy |||||  
Db 1201 CGCGACCATGGCACATGCTGTTCTTTATAGTCATCATCTTCCTAGGTTCAATCTATCTT 1260  
Qy |||||  
Db 1224 CGCGACCATGGCACATGCTGTTCTTTATAGTCATCATCTTCCTAGGTTCAATCTATCTT 1283  
Qy |||||  
Db 1261 GTGAATTTGATTTGGCCATTGTTGCCATGCTGTATGACGAATTCGAAGGAAGGCGGAA 1320  
Qy |||||  
Db 1284 GTGAATTTGATTTGGCCATTGTTGCCATGCTGTATGACGAATTCGAAGGAAGGCGGAA 1343  
Qy |||||  
Db 1321 GAAGAAGAGGCTCGCGAAGAGAGCGGATACGTGAAGCGGAAGAGCTGCCCGCGCCAAA 1380  
Qy |||||  
Db 1344 GAAGAGAGGCTCGCGAAGAGAGCGGATACGTGAAGCGGAAGAGCTGCCCGCGCCAAA 1403  
Qy |||||  
Db 1381 CGCGCCAAAGCTGGAGAGCGGGCCAAATCGCGAGGCTCAGGCAGCGAGGATGCGGCTGCC 1440  
Qy |||||  
Db 1404 CGCGCCAAAGCTGGAGAGCGGGCCAAATCGCGAGGCTCAGGCAGCGAGGATGCGGCTGCC 1463  
Qy |||||  
Db 1441 CGCGAAGAGGCTGCACCTGCATCCGGAATGCCAAGAGTCCGAGCTATCTTGGCATCAGC 1500  
Qy |||||  
Db 1464 CGCGAAGAGGCTGCACCTGCATCCGGAATGCCAAGAGTCCGAGCTATCTTGGCATCAGC 1523  
Qy |||||  
Db 1501 TATGAGCTATTGTTGGCGCGAGAAGGGCAACGATGACAAACAACAAGAGAAGATGTCC 1560  
Qy |||||  
Db 1524 TATGAGCTATTGTTGGCGCGAGAAGGGCAACGATGACAAACAACAAGAGAAGATGTCC 1583  
Qy |||||  
Db 1561 ATTGGAGCGCTGAGGTGAGATCGGAGTCGGTGTGAGCGGTTATACAAAGACACACGACCT 1620  
Qy |||||  
Db 1584 ATTGGAGCGCTGAGGTGAGATCGGAGTCGGTGTGAGCGGTTATACAAAGACACACGACCT 1643  
Qy |||||  
Db 1621 ACCACAGCACACCAAGCTACCAAGTTGCTAAAGTGGAGCAGCAGGCTTATACAAAGACAC 1662  
Qy |||||  
Db 1644 ACCACAGCACACCAAGCTACCAAGTTGCTAAAGTGGAGCAGCAGCAGCTTATACCTTACCT 1703  
Qy |||||  
Db 1663 -----TACACGATACGGAAC 1677  
Qy |||||  
Db 1704 GGTTCACCGTTTAACATACGAGGGATCAGTAGTTCTCACAGTACACGATACGGAAC 1763  
Qy |||||  
Db 1678 GGAGCTGCCCGCTTTGGTATACCGGCTAGCGATCGTAGCCATTGGTATGTCACATAT 1737  
Qy |||||  
Db 1764 GGAGCTGCCCGCTTTGGTATACCGGCTAGCGATCGTAGCCATTGGTATGTCACATAT 1823

Db 1738 CAGGATGCCAGCAGCAGCACTTGCCCTATGCGCAGCAGCTCGAATGCCGTACCCCGATGTCC 1797  
Qy |||||  
Db 1824 CAGGATGCCAGCAGCAGCACTTGCCCTATGCGCAGCAGCTCGAATGCCGTACCCCGATGTCC 1883  
Qy |||||  
Db 1798 GAAGAGAAATGGGCGCATCATAGTGCCTGTACTATGGCAATCTAGGCTCCCGACACTCA 1857  
Qy |||||  
Db 1884 GAAGAGAAATGGGCGCATCATAGTGCCTGTACTATGGCAATCTAGGCTCCCGACACTCA 1943  
Qy |||||  
Db 1858 TCGTATACCTTCGATCGATCCCGAATATCGTATACCTTCACATGGCGATCTACTCGGGGC 1917  
Qy |||||  
Db 1944 TCGTATACCTTCGATCGATCCCGAATATCGTATACCTTCACATGGCGATCTACTCGGGGC 2003  
Qy |||||  
Db 1918 ATGGCGTCAATGGCGTTCAGCACAATGACCAAGAGAGCAAAATGGCGAACCACACACA 1977  
Qy |||||  
Db 2004 ATGGCGTCAATGGCGTTCAGCACAATGACCAAGAGAGCAAAATGGCGAACCACACACA 2063  
Qy |||||  
Db 1978 CGCAATCAATCAGTGGGCGCCCAATGGGCGCACCCTGTCTGGACACCAATCAAG 2037  
Qy |||||  
Db 2064 CGCAATCAATCAGTGGGCGCCCAATGGGCGCACCCTGTCTGGACACCAATCAAG 2123  
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Db 2038 CTCGATCATCGCACTACGAAATTTGGCTGGAGTGCACGACGAAGCTGGCAAGATTAAA 2097  
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Db 2124 CTCGATCATCGCACTACGAAATTTGGCTGGAGTGCACGACGAAGCTGGCAAGATTAAA 2183  
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Db 2184 CATCATGACAATCCGTTTATTCGAGCCCGTCCAGACAAACGGTGGTGTGATGAAGAT 2243  
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Qy |||||  
Db 2244 GTGATGTCCTGAATGACATCATCGAACAGCGCGTGGTGGGACAGTGGGGAAGGAT 2303  
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Db 2304 CGCGGTCTCTCCGTTTACTATTTCCCAACAGAGAGCAGTACGAGGATGGCGGACGTTTC 2363  
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Db 2424 TGCTGGGTTTGGTTGAAATTTAGGAGTGGTATCGCTCATCTCTCGATCCCTTCGTC 2483  
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Db 2398 GAGCTCTTCATCAGCTGTGCATTTGGTCAACACGATGTTTCATGGCAATGGATCACCAC 2457  
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Db 2484 GAGCTCTTCATCAGCTGTGCATTTGGTCAACACGATGTTTCATGGCAATGGATCACCAC 2543  
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Db 2544 GATATGAACAAGGATGGAAACCGGTGCTCAAGAGTGGCAACTATTCTTCACCGCCACC 2603  
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Qy |||||  
Db 2604 TTTGCCATCGAGGCCACCATGAAGCTAAATGGCCATGAGCCCAAGTACTATTTCCAGGAG 2663  
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Db 2578 GGCTGGAACATCTTCGACTTCATTATCGTGGCCCTATTCGCTATTGGAACCTGGGACTCGAG 2637  
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Db 2664 GGCTGGAACATCTTCGACTTCATTATCGTGGCCCTATTCGCTATTGGAACCTGGGACTCGAG 2723  
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Db 2638 GGTGTCCAGGGTCTGCGGTTTGGGTTTCTTCGATTGCTGGGTGATTAACAAGTGGCC 2697  
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Db 2724 GGTGTCCAGGGTCTGCGGTTTGGGTTTCTTCGATTGCTGGGTGATTAACAAGTGGCC 2783  
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Qy |||||  
Db 2784 AAGTCTTGGCCACACATTAATTTACTCAITTCGATTATGGACGACCATGGCGCTTTG 2843  
Qy |||||  
Db 2758 GGTAAATCGACATTTGACTTTGCATTTATCATCTTTCGCGGTGATGGGAATGCAA 2817  
Qy |||||  
Db 2844 GGTAAATCGACATTTGACTTTGCATTTATCATCTTTCGCGGTGATGGGAATGCAA 2903  
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QY 2904 CTGTCGGAAGAAATATCATGATCACAGGACCGCTTCCGGATGGGACCTGCGCGCG 2963  
Db 2878 TGAACCTTACCAGCTTTATGACAGCTTTCATGATCGTGTCGGGTGCTCTCGGAGAA 2937  
QY 2964 TGAACCTTACCAGCTTTATGACAGCTTTCATGATCGTGTCGGGTGCTCTCGGAGAA 3023  
Db 2938 TGGATCGAGTCCATGTGGGACTGCATGTAGTGGGGGATGTCGTGCAATCCCTTCTTC 2997  
QY 3024 TGGATCGAGTCCATGTGGGACTGCATGTAGTGGGGGATGTCGTGCAATCCCTTCTTC 3083  
Db 2998 TTGGCCACCGCTTGCATCGGCAATCTTGCTGACTTAAACCTTTCTTAGCTTGCCTTTG 3057  
QY 3084 TTGGCCACCGCTTGCATCGGCAATCTTGCTGACTTAAACCTTTCTTAGCTTGCCTTTG 3143  
Db 3058 TCCAAATTTGGCTCACTAGCTTATCAGCGCCGACTGCGGATAACGATAGGAATAAATA 3117  
QY 3144 TCCAAATTTGGCTCACTAGCTTATCAGCGCCGACTGCGGATAACGATAGGAATAAATA 3203  
Db 3118 GCCGAGGCTTCAATCGAATTTGCCGATTTAAAGTTGGGTTAAGCGTAATATGCTGAT 3177  
QY 3204 GCCGAGGCTTCAATCGAATTTGCCGATTTAAAGTTGGGTTAAGCGTAATATGCTGAT 3263  
Db 3178 TGTTCGAAGTTAATACGTAACAAATGACAAATCAAAATAGTATGATCAACCATCAG---- 3232  
QY 3264 TGTTCGAAGTTAATACGTAACAAATGACAAATCAAAATAGTATGATCAACCATCAGGTGAG 3223  
Db 3233 -----AGCATGGTGACAAACGAACTGGAGCTG 3258  
QY 3324 AGGACCAACCAAGATCAGTTGGATTTGGAGCGAAGAGCATGCTGACAACTGGAGCTG 3383  
Db 3259 GGCACGACGAGATCTCGCCGAGCGGCTCATCAAGAAGGGGATCAAGAGGACGAGCAAA 3318  
QY 3384 GGCACGACGAGATCTCGCCGAGCGGCTCATCAAGAAGGGGATCAAGAGGACGAGCAAA 3443  
Db 3319 CTGAGGTGCCATCGGGGATGCGATGGAATTCACGATACACGCGACATGAGAACAAAC 3378  
QY 3444 CTGAGGTGCCATCGGGGATGCGATGGAATTCACGATACACGCGGACATGAGAACAAAC 3503  
Db 3379 AAGCCGAAGAAATCCAAATATCTAAATTAACGCAACG----- 3414  
QY 3504 AAGCCGAAGAAATCCAAATATCTAAATTAACGCAACGATGATTGGCAACTCAATTAACCAAC 3563  
Db 3415 -----GACGAGCAG 3423  
QY 3564 CAAGACAATAGACTGGAAACAGCAGCTAAACCATAGAGGTTTGTCTTTACAGGACGAGCAG 3623  
Db 3424 ACTGCCAGCATTAACCTCATATGCTAGCCATAAGAAATCGACCATTCAGGACGAGAGCCAC 3483  
QY 3624 ACTGCCAGCATTAACCTCATATGCTAGCCATAAGAAATCGACCATTCAGGACGAGAGCCAC 3683  
Db 3484 AAGGCGACGCCGAGAGCATGGAGGGCGAGGAAGCGCGACGCGCAAGAGGAGGATTTA 3543  
QY 3684 AAGGCGACGCCGAGAGCATGGAGGGCGAGGAGAGCGCGCCAGCAGAGGAGGATTTA 3743  
Db 3544 GGTCTCAGCAGGAGAACTGGACGAGGAGGGGGAATGCGAGGAGGGCGGCTCGACGGTGTAT 3603  
QY 3744 GGTCTCAGCAGGAGAACTGGACGAGGAGGGGGAATGCGAGGAGGGCGGCTCGACGGTGTAT 3803  
Db 3604 ATCAATTTATCATGCACACGACGAGGATATACTCGATGAATATCCAGCTGATTGCTGCCCC 3663  
QY 3804 ATCAATTTATCATGCACACGACGAGGATATACTCGATGAATATCCAGCTGATTGCTGCCCC 3863  
Db 3664 GATTCTGACTATAGAATAATTCGATCTTAGCCGCTGACGATGACTCGCGGCTTCTGGCAA 3723  
QY 3864 GATTCTGACTATAGAATAATTCGATCTTAGCCGCTGACGATGACTCGCGGCTTCTGGCAA 3923  
Db 3724 GGATGGGCAATTTACGACTGAAACCTTTTCGATTAATTTAGGATAAATATTTTGAACA 3783  
QY 3924 GGATGGGCAATTTACGACTGAAACCTTTTCGATTAATTTAGGATAAATATTTTGAACA 3983  
Db 3784 GCTGTTATCACTATGATTTAATGAGTAGCTTAGCTTTGGCATTTAGAAAGATGTACATCTG 3843  
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QY 3984 GCTGTTATCACTATGATTTTAAATGAGTAGCTTAGCTTTGGCATTAGAAAGATGTACATCTG 4043  
Db 3844 CCACAAGACCCTACTGCAAGGATATTTTATACTATATGACAGATAATTTTACGGTTATA 3903  
QY 4044 CCACAAGACCCTACTGCAAGGATATTTTATACTATATGACAGATAATTTTACGGTTATA 4103  
Db 3904 TTCTTCTTGGAAATGTTAATCAAGTGGTTGGCGCTCGGCTTCAAAGTGTACTTGACCAAC 3963  
QY 4104 TTCTTCTTGGAAATGTTAATCAAGTGGTTGGCGCTCGGCTTCAAAGTGTACTTGACCAAC 4163  
Db 3964 GGGTGGTGTGGCTCGATTTCTGATTGTCATGGTATCGCTTATCAACTTCGTTGCTTCA 4023  
QY 4164 GGGTGGTGTGGCTCGATTTCTGATTGTCATGGTATCGCTTATCAACTTCGTTGCTTCA 4223  
Db 4024 CTTGTTGGAGCTGGTGGTATTCGAAGCTTCAAGACTATCGAAGCTTAAAGACACTGAGA 4083  
QY 4224 CTTGTTGGAGCTGGTGGTATTCGAAGCTTCAAGACTATCGAAGCTTAAAGACACTGAGA 4283  
Db 4084 CCACCTACGTCGCCATGTCCTGATGAGGCGATGAGGGTCTGCTTAATGCGCTGGTACAA 4143  
QY 4284 CCACCTACGTCGCCATGTCCTGATGAGGCGATGAGGGTCTGCTTAATGCGCTGGTACAA 4343  
Db 4144 GCTATACCGTCCCATCTTCAATGTGCTATTGGTGTGCTAATATTTTGGCTAATTTTGGC 4203  
QY 4344 GCTATACCGTCCCATCTTCAATGTGCTATTGGTGTGCTAATATTTTGGCTAATTTTGGC 4403  
Db 4204 ATAATGGGTGTACAGCTTTTCTGGAAATATTTTAACTGCGAGGACATGAATGCGACG 4263  
QY 4404 ATAATGGGTGTACAGCTTTTCTGGAAATATTTTAACTGCGAGGACATGAATGCGACG 4463  
Db 4264 AGCTCAGCAGAGATCATACAAATCGCAATGCTCGGAGAGCGAGAACATACAGCTGG 4323  
QY 4464 AGCTCAGCAGAGATCATACAAATCGCAATGCTCGGAGAGCGAGAACATACAGCTGG 4523  
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QY 4524 GTGAATTCAGCAATGAATTCGATCATGTAGTGAACGCTATCTGTCCTTTTCCAAAGTG 4583  
Db 4384 GCCACCTTCAAAGGCTGGATACAAATCATGAACGATGCTATCGATTACAGAGAGTGGAC 4443  
QY 4584 GCCACCTTCAAAGGCTGGATACAAATCATGAACGATGCTATCGATTACAGAGAGTGGAC 4643  
Db 4444 AAGCAACCAATTCGTTGAAAGCAACATCTACATGATTTTATTTATTTCTTCATCATTA 4503  
QY 4644 AAGCAACCAATTCGTTGAAAGCAACATCTACATGATTTTATTTATTTCTTCATCATTA 4703  
Db 4504 TTTGGATCATTTTTCACATCAATCTGTCATGTTGTTATCATCTATCTATTTTATGAG 4563  
QY 4704 TTTGGATCATTTTTCACATCAATCTGTCATGTTGTTATCATCTATCTATTTTATGAG 4763  
Db 4564 CAAAAGAAAAAGCAGGTGGATCATTTAGAAATGTTTCATGACAGAAGATCAGAAAAAGTAC 4623  
QY 4764 CAAAAGAAAAAGCAGGTGGATCATTTAGAAATGTTTCATGACAGAAGATCAGAAAAAGTAC 4823  
Db 4624 TATAGTGTATGAAAAAGATGGGCTCTAAAAACCATTTAAAGCCATTTCCAGACCAAGG 4683  
QY 4824 TATAATGCTATGAAAAAGATGGGCTCTAAAAACCATTTAAAGCCATTTCCAGACCAAGG 4883  
Db 4684 TGGCGACCACAAAGCAATAGTCTTTGAAATAGTAACCGATAAGAAATTCGATATAATCATTT 4743  
QY 4884 TGGCGACCACAAAGCAATAGTCTTTGAAATAGTAACCGATAAGAAATTCGATATAATCATTT 4943  
Db 4744 ATGTTATTCATTTGGTCTGAACATGTTTACCACCTCGATGTTACGATGCTGCGGAC 4803  
QY 4944 ATGTTATTCATTTGGTCTGAACATGTTTACCACCTCGATGTTACGATGCTGCGGAC 5003  
Db 4804 ACGTATAACCGCGTCTAGACTATCTCAATCGGATATTCGTAGTATTTTTCAGTTCCGAA 4863  
QY 5004 ACGTATAACCGCGTCTAGACTATCTCAATCGGATATTCGTAGTATTTTTCAGTTCCGAA 5063  
Db 4864 TGTCTATTAATAATATTCGTTTACGATATCTATTTTATGAGCATGGAATTTATTT 4923  
QY 5064 TGTCTATTAATAATATTCGTTTACGATATCTATTTTATGAGCATGGAATTTATTT 5123  
|||||



Db	931	CACAAATAGCAACAGTTTCCAAATTTGGTTTTACGGAGAACGATGCGGAGTCAATATTCGGGTGTGC	990
Qy	987	CAAAATCGCAATAGCTTCCAAATTTGGTATTCCGAGGACGAGGCATCTCTCAATTTCCGTTATGC	1046
Db	991	GGAAATGATTCGGGTGCGGACAATTCGCGCAGGAGTATACGTCTCCCTGTCAGGCGTCTCGGC	1050
Qy	1047	GGCAATATATCCGGTTCGGGGCAATTCGACGACGATTAACGTGTGCCCTGTCAGGGGTTTGGT	1106
Db	1051	CCCAATCCCAACTACGACTACACCAAGTTTTCGATTTCATTTCCGTTGGGCTTTCCCTGTCCGGCG	1110
Qy	1107	CCGAATCCGAATTTATGGCTACACCAAGCTTCGATTTCGTTCCGATGGCTTCTTCTGTCTCGGCC	1166
Db	1111	TTTCGTCTCATGACCCAAAGATTTCTGGGAGGATCTGTATACGACAGCTGTCTGTCGAAGCAGCT	1170
Qy	1167	TTCCGGCTGATACACAGGACTTCTGGGAGGATCTGTACCAAGCTGGTGTTCGCGCGCGCC	1226
Db	1171	GGACCTGGCACATGTTGTTCTTTATAGTCATCATCTTCCTAGCTTCATATCTATCTGTGTG	1230
Qy	1227	GGACCATGGCACATGCTGTCTTTATAGTCATCATCTTCCTAGGTTTCATATCTATCTTGTG	1286
Db	1231	AATTTGATTTTGGCCATTGTTGCCATGTCTTATGACGAATTTGCAAAAGAAAGGCCGCAAGAA	1290
Qy	1287	AATTTGATTTTGGCCATTGTTGCCATGTCTGATGACGAATTTGCAAGGAAGGCCGCAAGAA	1346
Db	1291	GAGAGGCTGCCGAGGAGGAGCGATACGAGAAGCTGAAGAAGCGGACGAGCCAGCCAAAGCG	1350
Qy	1347	GAAAGGCTGCCGAGGAGGAGCGATACGTGAAGCGGAAGAAGCTGCCGCCGCAAGCG	1406
Db	1351	GCCAACTGGAGAGCGGCCAATGTAGCAGCTCAAGCGGCTCAGGATCGACGCGGATGCC	1410
Qy	1407	GCCAACTGGAGAGCGGCCAATGCGCAGGCTCAGGACGAGCGGATCGGGCTGCGCGCC	1466
Db	1411	GCTCGCGCAGCTCTGCATCCGAGATGGCAAGAGTCCCAAGTACTCTTGCATTAGCTAT	1470
Qy	1467	GAAAGGCTGCATGCTATCCGGAATGGCCAGAGTCCGACGTATCTTGCATCAGCTAT	1526
Db	1471	GACTGTTTGTTCGGCGGAGAAAGGCAACGATGACAAACAACAAGAGAAGATGTCATA	1530
Qy	1527	GAGCTATTTTGGCGCGGAGAAGGCAACGATGACAAACAACAAGAGAAGATGTCATT	1586
Db	1531	CGCAGGCTCGAAGTGAATTCGGAGTCGGTGACGCTTATACAAAGCACACGACCTTACC	1590
Qy	1587	CGAGAGGCTCGAGTGGAGTCCGAGTCGGTGACGCTTATACAAAGCACACGACCTTACC	1646
Db	1591	ACAGCAC - CG - -GCTACTAAAGTCGGTAAAGTTTACGACGACTTCTCTATCCTTACCTGGT	1647
Qy	1647	ACAGCACACCAAGCTACCAAGTTTCGTAAGTGCACAGCATCCTTATCCTTACCTGGT	1706
Db	1648	TCACCATTTAACCTACGCGGGGATCACGTAGTTTCACACAAAGTACACAATACGAATATCG	1707
Qy	1707	TCACCGTTTAAACATACGCGGGGATCACGTAGTTTCCTACAAGTACACGATACGGAACGGA	1766
Db	1708	CGTGGACGTTTTGGTATACGAGGTAGCGATCCGACGCCATTGGTACTGTCGAACAATATCAG	1767
Qy	1767	CGTGGCGCTTTTGGTATACCGGTAGCGATCTGTAAGCATTGGTATTTGTCACAATATCAG	1826
Db	1768	GATGCCCAGCAGCATTTGCCCTATGCCGATGACTCGAATGCCGTAAACCAATGTCGGA	1827
Qy	1827	GATGCCCAGCAGCATTGCCCTATGCCGACGACTCGAATGCCGTACCCCGATGTCGGA	1886
Db	1828	GGAATGGTGCCATTATGTATCCAGGCTACTATTGTAATTTAGGTTCTAGACATCTTCA	1887
Qy	1887	GAGAAATGGGCCCATCATAGTGGCCGTTACTATGGCAATCTAGGCTCCGACATCATCG	1946
Db	1888	TATACCTTCGATCAATCAGAAATCTCGTATACATCAGTGTGATTTATGGGTGGCGATG	1947
Qy	1947	TATACCTTCGATCAGTCCCGAATATCGTATACCTCAGATGGCGATCTACTCGCGGGCATG	2006
Db	1948	CGCGCCATGGTGCCAGCACATGATCCAAAGAGCAAAATGCCAGTTCGCAACACACGC	2007
Qy	2007	GCCCTATGGGCGTCAGACAAATGACCAAGGAGAGCAAAATTCGCGAACCGCAACACACGC	2066
Db	2008	AATCAATCAATCGGTGCTGCAACCAATGCTGSCAGTACTAGGCTGGTGGTGGCTATCCC	2067

[illegible]



Db	5245	ATCTTTGCTATCTTTGGCATGTCCTTCTTCATGCATGTCAAAGAGAGAGACGGCGATAAAT	5304
QY	5349	ATCTTTGGCCATTTTGGCCATGTGCTTCTTCATGCACGTGAAGGAGAGACGGCGATTAAC	5408
Db	5305	GCTGTGTATAATTTTAAAGACATTTGGCCAAAGTATGATATGCTGTTTCAGATGCTACC	5364
QY	5409	GAGCTCTACAACCTTCAAGACCTTTGGCCAGACATGATCTTGCTTTCAGATGCTCAGC	5468
Db	5365	TCAGCCGGTTGGGATGGTGTGTAGATGCCATTATCAATAGGAAAGATTTGGCATCCACC	5424
QY	5469	TCAGCCGGTTGGGATGGTGTACTGGACGCCATTATCAATAGGAAGCATGCGATCCACC	5528
Db	5425	GACAACGACAAAGGCTATCCGGGCAATTTGGTTCAGCGACTGTTGGAATTTACGTTTCTC	5484
QY	5529	GACAGCGACAAAGGCTATCCGGGCAATTTGGTTCAGCGACCGTTGGAATTAACGTTTCTC	5588
Db	5485	CTTTCATATCTAGTTATAAGCTTTTGTAGTATTAAATATGTACATTTGCTGTCATTCTC	5544
QY	5589	CTCTCATCTAGTTATAAGCTTTTGTAGTATTAAATATGTACATTTGCTGTCATTCTC	5648
Db	5545	GAGAACTATAGCCAGCTACGGAGGATTCACAGGAGGCTCTCACCGACGAGATTAGAT	5604
QY	5649	GAGAACTATAGTCAGGCCACCGAGGACGTGCAAGAGGCTTAACCGACGAGCTACGAC	5708
Db	5605	ATGTACTACGAGATTTGGCAACAATTCGATCCGGAGGCGACCCAGTACATACGCTACGAC	5664
QY	5709	ATGTACTATGAGATCTGGCAGCAATTCGATCCGAGGGCCACCCAGTACATACGCTATGAT	5768
Db	5665	CAGCTGTCGAGTTTCTGCACTGTGAGCGCCGCTGCGAGATCCACAACCGCAACAG	5724
QY	5769	CAGCTGTCGAAATTCCTGGACGCTACTGGAGCCCCGCTCGAGATCCACAAAACCGAACAAG	5828
Db	5725	TACAAAATCATATCGATGACATGCCGATATCTCGGGCGACATGATCTACTGTGTGGAT	5784
QY	5829	TACAAGATCATATCGATGACATACCCATCTCTCGCGGTGACCTCATGTACTGCGTGCAC	5888
Db	5785	ATATTGGATGCCCTGACCAAGGACTTCTTTGGCGCAAGGGTAAATCCGATCGAGGAGACG	5844
QY	5889	ATCCTCGAGCGCCCTTACGAAAGACTTCTTTGCGCGGAAGGGCAATCCGATAGAGGAGACG	5948
Db	5845	GGTGAATTTGGTAGATACGGCGGACCGGACCCGAGGCGCTATGATCCGGTCTCGTCA	5904
QY	5949	GGTAGATTTGGTAGATACGGCCGCCCGGATACGGAGGGCTACGAGCCCGTCTCATCA	6008
Db	5905	ACACTGTGCGCCACCGTGAAGGAGTACTGCGCCAAAGCTGATACAGAATTCGCTGGCG	5960
QY	6009	ACSGTGTGGCGTCAAGCGTGAGGAGTACTGCGCCCGGCTAATCCAGACGCGCTGGCG	6064

RESULT	6	
ID	US-08-772-512A-1	STANDARD; DNA; UNC; 6318 BP.
AC	xxxxxx	
DT		
DE	Sequence 1,	Application US/08772512A
CC	Sequence 1,	Application US/08772512A
CC	GENERAL INFORMATION:	
CC	APPLICANT:	Soderlund, David M.
CC	APPLICANT:	Knipples, Douglas C.
CC	APPLICANT:	Ingles, Patricia J.
CC	TITLE OF INVENTION:	INSECT SODIUM CHANNELS FROM
CC	TITLE OF INVENTION:	INSECTICIDE-SUSCEPTIBLE AND INSECTICIDE-RESISTANT HOUSE
CC	TITLE OF INVENTION:	FLIES
CC	NUMBER OF SEQUENCES:	19
CC	CORRESPONDENCE ADDRESS:	
CC	ADDRESS:	NIXON, HARGRAVE, DEVANS & DOYLE LLP
CC	STREET:	P.O. Box 1051, Clinton Square
CC	CITY:	Rochester
CC	STATE:	New York
CC	COUNTRY:	USA
CC	ZIP:	14603
CC	COMPUTER READABLE FORM:	
CC	MEDIUM TYPE:	Floppy disk
CC	COMPUTER:	IBM PC Compatible

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CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/772,512A
CC FILING DATE:
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/608,618
CC FILING DATE: 01-MAR-1996
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Braham, Susan J.
CC REGISTRATION NUMBER: 34,103
CC REFERENCE/DOCKET NUMBER: 19603/601(CRFD-1657)
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 716-263-1636
CC TELEFAX: 716-263-1600
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 6318 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: CDNA
CC SEQUENCE 6318 BP: 1713 A; 1341 C; 1597 G; 1667 T; 0 OTHER.

Query Match 56.4%; Score 3676; DB 20; Length 6318;
Best Local Similarity 84.9%; Pred. No. 0.00e+00;
Matches 4986; Conservative 0; Mismatches 806; Indels 84;
Caps 21;

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Db 811 CTGTCGGTTCGCGCTGATGGGCTCAAAATCTATATGGTGTCTTAACACAAAAGTGC 870  
QY 867 CTGTCGGTTCGCGTGTATGGGCTTACAGATCTATATGGGCTGCTCACCGAGAGTGC 926  
Db 871 ATTAACAGATTCCTCCCTGGACGGCAGTGTGGGCAATCTGACGATGAAATGGTTCCTA 930  
QY 927 ATCAAGAAGTTCCTCCCTGGACGGTTCCTGGGCAATCTGACCGACGAGAATGGGACTAT 986  
Db 931 CACATAGCAACAGTTCCTCAATTTGGTTACGGAGAACGATGGGAGTCAATCCGGTGTGC 990  
QY 987 CACAATCGCAATAGTCTCAATTTGGTATTCGGAGGACGAGGCAATCTCAATTTCCGTTATGC 1046  
Db 991 GGAATGTATCCGGTCCGGCAATTCGGCGAGGATTAAGTCTGCTGCTGACAGGCTTCGCG 1050  
QY 1047 GGCATATATCCGGTCCGGGCAATTCGGACGACGATTAAGTGTGCTGCAGGGTTTGGT 1106  
Db 1051 CCCAATCCAACTACGACTACACCAAGTTTCGAGTTTCGATTCATTCGGTGGGCTTCCTGTGCGCG 1110  
QY 1107 CGCAATCCGAATTTATGGCTACACCAAGTTCGATTCGGTTCGGATGGGCTTCCTGTGCCGCC 1166  
Db 1111 TTTCGCTCATGACCAAGATTTCTGGGAGGATCTGTATCAGCAGCTGCTGCAACGAGCT 1170  
QY 1167 TTCGGCTGATGACACAGGACTTCTGGGAGGATCTGTACCACTGGTGTGCGCGCCGCC 1226  
Db 1171 GGACCTGCGACATGTGTCTTTATAGTCATCATCTTCTAGGTTCAATCTATCTTGTG 1230  
QY 1227 GGACATGGCAGATGTGTCTTTATAGTCATCATCTTCTAGGTTCAATCTATCTTGTG 1286  
Db 1231 AATTTGATTTTGGCCATGTGTGCCATGTCTTATGAGCAATTCGAAAGAACGCCGAAGAA 1290  
QY 1287 AATTTGATTTTGGCCATGTGTGCCATGTCTGATGAGCAATTCGAAAGAACGCCGAAGAA 1346  
Db 1291 GAAGAGCTGCCGAGGAGGCGGATACGAGAGCTGAAGAGCGGACGACGCCAAGGCG 1350  
QY 1347 GAAGAGCTGCCGAGGAGGCGGATACGAGAGCTGAAGAGCGGACGACGCCAAGGCG 1406  
Db 1351 GCCAACTGGAGGAGGCGGCAATGTAGCAGCTCAAGCGGCTCAGGATGACGCGATGCC 1410  
QY 1407 GCCAAGCTGGAGGAGGCGGCAATGCGCAGGCTCAGGACGACGCGATGCGCTGCCGCC 1466  
Db 1411 GCTGGCGCAGCTCTGATCCGAGATGGCAAGAGTCCACAGTCTTTCGATTAAGTAT 1470  
QY 1467 GAAGAGCTGCATGCTATCCGAAATGGCCAAAGTCCGACGATTTCTTGCATCAGCTAT 1526  
Db 1471 GAATGTTTGTGGCGGAGAGGCGCAACGATGACAAACAAAGAGAGATGTCCATA 1530  
QY 1527 GAGCTATTTGTGGCGGAGAGGCGACGATGACAAACAAAGAGAGATGTCCATT 1586  
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QY 1587 CGGAGCGTCGAGGTGGAGTCGGAGTCGGTGGAGCGTTATACAAAGACACAGCACCTACC 1646  
Db 1591 ACAGCAC-CC-GCTACTAAGTCCGTAAGTTAGCAGGACTTCCTTATCCTTACCTGCT 1647  
QY 1647 ACAGCACCAAGCTACCAAGTTCCGTAAGTGGACGACGATCCTTATCCTTACCTGCT 1706  
Db 1648 TCACCAATTAACCTACCGCGGATACAGTACAGTTCACAAAGTACACAATACGAAATGGG 1707  
QY 1707 TCACCGTTTAAATACACCGCGGATACAGTACAGTTCACAAAGTACAGTACGAAACGGA 1766  
Db 1708 CGTGGAGCTTTTGGTATACAGGTAGCGATCGCAAGCCATTGGTACTGTGCAACATATCAG 1767  
QY 1767 CGTGGCGCTTTGGTATACCGGTAGCGATCGTAAAGCAATTTGTTGTCAACATATCAG 1826  
Db 1768 GATGCCAGCAGCAATTTGCCCTATGCCGATGACTCCGAATCCGCTAACCAATGTCGGA 1827  
QY 1827 GATGCCAGCAGCAATTTGCCCTATGCCGATGACTCCGAATCCGCTAACCAATGTCGGA 1886  
Db 1828 GAGATGGTGCATATATAGCAGGCTACTATTTGTAATTTAGGTTCTTAGACATTTCTCA 1887  
QY 1887 GAGAAATGGGCGCATCATATGCGCGTGTACTATGGCAATCTAGGCTCCCGCAGACACTCATG 1946  
Db 1888 TATACCTCGGCATCAATCAAGAAATCTCGTATACATCAGATCGTGTATTTATTTGGGTGGCATG 1947

QY 1947 TATACCTCGCATCAGTCCCGAATATCGTATACATCGGATCTACTCGCGGCATG 2006  
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QY 2007 GCCGTATGGGCTGACGACAATGACCAAGGAGAGCAAAATGGCAACCGCAACACACCG 2066  
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QY 2067 AATCAATCAGT-GG-GC-GCCACCAATGGCGGACCA--C-CTG-TC-TGGACA--CC 2114  
Db 2068 GATGCCAATCACAAAGAACAAAGGATATGAAATGGTTCAGGATTTATACAGACGAAGCT 2127  
QY 2115 AATCACAAAGCTC--GATCATCGGACTACGAAATTTGGCTGGAGTGCACGGACGAAGCT 2171  
Db 2128 GGCAAAATAAACACACGACGACAAATCTTTTATCGAGCCGCTCCAAACTCAAAACAGTGGTA 2187  
QY 2172 GGCAAAGATTAACATCATGACAAATCTTTTATCGAGCCGCTCCAGACACAAACGGTGGTT 2231  
Db 2188 GACATGAAGATGTATGGTCTTAAATGATATCATTTGAACAAGCCGCTGTCGCGCATAGT 2247  
QY 2232 GATATGAAGATGTATGGTCTTGAATGACATCATCGAACAGCCGCTGGTCCGACAGT 2291  
Db 2248 CGTCTAGTGAACGAGAGTG-----AGGACGATGACGAGAGT 2283  
QY 2292 CGGCAAGCGATCGCGGTGTCTCGTTTACTATTTCCAAACAGAGGACGATGACGAGAT 2351  
Db 2284 GGTCCACATTCAGGACATCGCCCTCGAATACATCTCTAAAGGCATCGAAATCTTTGT 2343  
QY 2352 GGGCGGAGTTCAAAGACAAAGGCACTCGAAGTATCTTCAAGGCAATCGATGTGTGTGT 2411  
Db 2344 GTATGGGAGCTGTTGTTGGTGTGTTAAAAATTTCAAGAAATGGGTGTCCTTTATTTGTGTT 2403  
QY 2412 GTGTGGGAGCTGTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2471  
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QY 2472 GATCCCTTCGTGAGCTCTTCATCACGCTGTGATTTGTTGTTCAACAGATGTTTCATGGCA 2531  
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QY 2532 ATGATCACAGATATGAACAGAGATGGAAGCGCTGTCTAAGATGGCACTATTTTC 2591  
Db 2524 TTCACGGCGACTTTTGGCAATTTGAAGCAGCATGAACATGATGGCCATGAGCCCGAAGTAC 2583  
QY 2592 TTCACGGCGACTTTTGGCAATTCGAGGCCACCATGAAGCTAATGGCCATGAGCCCGAAGTAC 2651  
Db 2584 TACTTCCAGGAGGCTGGAACATTTTCGATTTTCATTTGTTGCTTGTCTGCTGCGAA 2643  
QY 2652 TATTTCAGGAGGCTGGAACATTTTCGATTTTCATTTGTTGCTTGTCTGCTGCGAA 2711  
Db 2644 TTGGCCCTGGAGGCTGTCAGGCGCTGTGCGTGTGAGAAATTTTCGTTGCTTGTGCTGTA 2703  
QY 2712 CTGGAGCTGAGGCTGTCAGGCTGTGTCGATTTGCGTTCCTTTTCGATTTGCTGCGTGA 2771  
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QY 2772 TTCAAATTTGGCAAAATCTTGGCCACACTTAAATTTACTCATTTTCGATTTAGGGACGACC 2831  
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QY 2832 ATGGGCGCTTTGGGTAATCTGACATTTGCTTGTGCTTATCATCTCTTTCGCGGTG 2891  
Db 2824 ATGGGAATGCAACTTTTCGAAAGAACTATATTGACCACAAAGGATCGCTTCAAGGACCAT 2883  
QY 2892 ATGGGAATGCAACTGTTCGAAAGAAATTTATCATGATCACAAGGACCGCTTTCCGAGTGC 2951  
Db 2884 GAATTTACCGCGTGAACCTTCACCGACTTCATGACAGCTTCATGATGTTGTTCCGAGTG 2943  
QY 2952 GACCTTCGCGCGTGGAACTTCACCGACTTTATGACAGCTTCATGATGTTGTTCCGGGTG 3011  
Db 2944 CTGTGCGGAGAGTGGATCGAGTCCATGTGGGACTGCTATGTATGTTGGGCGATGTGACGTGT 3003







QY 747 TTTAGGTCGTCGAGCGCTTAAACCGTAGCCATTGTGCCAGCGCTTGAAGACCATCGTC 806  
Db 751 GGTGCTGTCATTGAATCTGTAAAAATCTACGGGATGTGATAATTTTGACAAATGTTTCC 810  
QY 807 GCGCGCTCATCGAATCGGTGGAAGATCTCGCGATGTGATTATCTCGTACCATGTTCTCC 866  
Db 811 CTCTCGGTGTTCCGCTGATGGGCTTACAAATCTATATGGGTGTTCTAACACAAAAGTGC 870  
QY 867 CTCTCGGTGTTCCGCTGATGGGCTTACAGATCTATATGGGCTGTCTACCGGAGAGTGC 926  
Db 871 ATTAACAGGATTTCCCTTGGACGCGAGTTGGGCAATCTGACCCGATGAAGAACTGTTTCTA 930  
QY 927 ATCAAGAGTTCCCGCTGGACGCTTCTGGGGCAATCTGACCGACGAGAACTGGGACTAT 986  
Db 931 CACAATAGCAACAGTTCCAAATGTTTACGAGAACGATGGCGAGTCAATACCGGTGTC 990  
QY 987 CACAATCGCAATAGTCCAAATGTTATTCGAGGACGAGGCGATCTCATTTCCGTTATGC 1046  
Db 991 GGAATGTATCCGGTGGGGGACAAATGGGGGAGGATTTACGTCTGCGTGCAGGCTTCGGC 1050  
QY 1047 GGAATATATCCGGTGGGGGCAATGCGACGAGATTACGTGTCCCTGAGGGGTTTGGT 1106  
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QY 1227 GGACCATGGCACATGTTGTTCTTTATAGTCATCATCTTCCTAGGTTCAATTCATCTTGTG 1286  
Db 1231 AATTTGATTTTGCCATTGTTGCCATGCTCTATGACGAATGCAAAAGAGCGCGAAGAA 1290  
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Db 1411 GCTCGCGCAGCTCTGCATCCGAGATGGCAAGAGTCCCAAGTCTCTTGCATTAGCTAT 1470  
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Db 1708 CGTGACGTTTGGTATACCGATAGCGATCGCAAGCCATTGGTACTGCAACATATCAG 1767  
QY 1767 CGTGCGGCTTTGGTATACCGGTAGCGATCGTAAGCCATTGTAATGTCAACATATCAG 1826  
Db 1768 GATGCCCAGCAGCATTTGGCCCTATGCGGATGACTCGAATGCCGTACACCAATGTCGGAA 1827  
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Db 1828 GGAATGTTGGTCCATTATAGTACCAGCCTACTATTGTAATTTAGGTTCTAGACATTTCTCA 1887  
QY 1887 GGAATGTTGGCCATCATAGTGCCTGTACTATGCAATCTAGGCTCCCGACACTCATCG 1946  
Db 1888 TATACCTCCGATCAATCAAGAAATCTCGTATACATACATGTTGTTATTTGGTGGCATG 1947  
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Db 1948 GGGCCATGGTGGCAGCACAATGACCAAGAGAGCAAAATTCGCGAGTCGCAACACACGC 2007  
QY 2007 GCGTCATGGGCGTCAGCACAAATGACCAAGGAGAGCAAAATTCGCGAACCGCAACACGC 2066  
Db 2008 AATCAATCAATCGGTGCTGCAACCAATGTTGGCAGTAGTACGGCTGGTGGTGGCTATCC 2067  
QY 2067 AATCAATCAGT--GG--GCCACCAATGCGGCACCA--C--CTG--TC--TGGACA--CC 2114  
Db 2068 GATGCCAATCAACAAGAACAAAGGATTTATGAATGGGGTCAGGATTTATACAGACGAAGCT 2127  
QY 2115 AATCAACAAGCTC--GATCATCGGACTACGAATTTGGCTGGAGTGCAGGACGAAGCT 2171  
Db 2128 GCAAAATAAAACACCACGACCAATCTTTATCGAGCCGCTCCAACTCAACACAGTGGTA 2187  
QY 2172 GCAAGATTAACATCATGACAATCTTTATCGAGCCGCTCCAGACACAAACGTTGGTT 2231  
Db 2188 GACATGAAGATGTTATGTTCTTAAATGATATCATTTGAACAGCCGCTGGTGGCATAGT 2247  
QY 2232 GATATGAAGATGTTATGTTCTCTGAATGACATCATGCAACAGCCGCTGGTGGCACAGT 2291  
Db 2248 CGTGTAGTGAACGAGGTG-----AGGACGATGACGAAGAT 2283  
QY 2292 CGGGCAAGCATCGCGCTGTCTCCGTTTACTATTTCCCAACAGAGGACGATGACGAGAT 2351  
Db 2284 GTTCCACATTAAGGACATCGCCCTCGAATACATCTTAAAGGCTCAAAATCTTTTGT 2343  
QY 2352 GGGCCGACGTTTCAAGACAAAGGACCTCGAAGTGAATCTTCAAGGCAATGATGTTTGT 2411  
Db 2344 GATGGGACTGTTGTTGGTGTGTTTAAATTTTCAAGAAATGGGTGCTCTTTATTTGTTTC 2403  
QY 2412 GTTGGGACTGTTGCTGGGTTTGGTTGAATTTTCAAGAGTGGTATCGCTCATCGCTTC 2471  
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QY 2472 GATCCCTTCGTGGAGCTTTCATACGCTGTGCTATGTTGGTCAACACGATGTTTCATGGCA 2531  
Db 2464 ATGGATCATCAGCAGATGAATCCGGAATTAGAGAAGTCTGGAAGTGGTAACTATTTTC 2523  
QY 2532 ATGGATCACCCAGATATGAACAAAGGAGATGGAAACGCTGCTCAAGAGTGGCACTATTTTC 2591  
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QY 2592 TTCACGGCCACTTTGCCATCGAGGCCACCATGAAGCTAATGGCCATGAGCCCCAAGTAC 2651  
Db 2584 TACTTCCAGAAAGGCTGGAAACATTTTCGATTTTCATTTATTTGGCTTGTCTCTGCTGAA 2643  
QY 2652 TATTTCCAGAGGGCTGGAAACATCTTCGACTTCATTTATCGTGGCCCTATCGCTATTGGAA 2711  
Db 2644 TTGGGCTCGAGGGTCTCAGGGCTGTGGTGTGAGAAGTTTTCGTTGTTGTTCTGCTGTA 2703  
QY 2712 CTGGGACTCGAGGGTCTCAGGGTCTGCTCGGTTATTCGTTCTCTTTCGATTGTCGCTGTA 2771  
Db 2704 TTCAAATTTGGCAAAATCATGGCCACACATTTACTTACTTTCATTTTCGATTATGGCCGAGCA 2763  
QY 2772 TTCAAACTGGCCAAAGTCTTGGCCACACATTAATTTACTCATTTTCGATTATGGGACGACC 2831  
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QY 2892 ATGGGAATGCACTTTTCGGAAGAAGAAATTTATCATGATCACAAGGACCGCTTTCGGGATGCG 2951



QY	5109	CCATGGAATTTATTGCAATGCTAGTGTGCTATTTTATCCATCTCTAGGCTTGTGACTTAGC	5169
Db	5065	GACATCATTTGAGAAGTATTTTCGTATCGCGCAGACACTGCTCCGCTGGTGGAGAGTGGCCAAA	5124
QY	5169	GATATTATCGAGAAGTACTTCTGTGTCGCGACCCCTGCTCCGAGTGGTGGTGTGGCGAAA	5228
Db	5125	GTGGGTGCTGCTCGGTTTACTCAAGGGTGCCAAAGGATATCCGGACGTTGCTGTGTCGG	5184
QY	5229	GTGGGCGGTGCTTTCGACTGTGTGAAGGAGGCCAAGGCGCATTCGGACACTGCTCTTTCGG	5288
Db	5185	TTAGCCATCTGCTGCTCGCTTATTCAACATTTGCTGTGCTGTCTTGGTGATGCTTC	5244
QY	5289	TTGGCCATCTGCTGCTGGCGCCCTGTTCACACTCTGCCCTGCTGTCTTCCCTGGTCATGCTC	5348
Db	5245	ATCTTTGCTATCTTTGGCATGCTCCTTCTCATGCTATGCAAGAGAGAAGCGGCATAAAT	5304
QY	5349	ATCTTTGCCATTTTCGGCATGTCGTTCTTCATGCACTGAAGGAGAGAAGCGGCATTAAC	5408
Db	5305	GCTGTGTATAATTTTAAGACATTTTGCCCAAAGTATGATATTGCTGTGTTTCAGATGTCTACC	5364
QY	5409	GAGCTCTACAAGCTTCAAGACCTTTGGCCAGAGCATGATCCTGCTCTTCAGATGCTCGACG	5468
Db	5365	TCAGCCGGTTGGGATGGTGTGTAGATGCCATTAATCAGTAGGAGAAGTATCGGATCCACCC	5424
QY	5469	TCAGCCGGTTGGGATGGTGTACTGAGCGCCATTAATCAATAGGAAAGCATGCGATFCCACCC	5528
Db	5425	GACAACGACAAGGGCTATCCGGGCAATTTGGTTCAGGCACTGTTGGAATTAAGTCTTC	5484
QY	5529	GACAGCGACANAAGGCTATCCGGGCAATTTGGTTCAGCGACCGTTGGANAACGTTTCTC	5588
Db	5485	CTTTCATATCTAGTTATAAGCTTTTTTGATAGTATTAATATGTACATTGCTGTCATTTCTC	5544
QY	5589	CTCTCATACCTAGTTATAAGCTTTTTTGATAGTATTAATATGTACATTGCTGTCATTTCTC	5648
Db	5545	GAGAACTATATCCAGCGCTACGAGAGATGTACAGAGGGTCTACCGGAGGAGATTACGAT	5604
QY	5649	GAGAACTATAGTCAGGCCACCGAGGACGTGCAAGAGGGTCTAAACCGCAGCAGACTACGAC	5708
Db	5605	ATGTACTACGAGATTTGGCAACAATTCGATCCGGAGGACCCACAGTACATACGCTACGAC	5664
QY	5709	ATGTACTATGAGATCTGGCAGCAANTTCGATCCGGAGGACCCACAGTACATACGCTATGAT	5768
Db	5665	CAGCTGTCCGAGTTTCTGGACGTGCTGGAGCCGCGCTGCAGATCCCAACGCGGAACAAG	5724
QY	5769	CAGCTGTCCGAAATCTCTGACGCTACTGGAGCCCCGCTGCAGATCCCAACCGAACAAG	5828
Db	5725	TACAAAATCATATCGATGACATGCCGATATGTCGGGGCGACATGATGTACTGTGTGGAT	5784
QY	5829	TACAAAGTATATATCGATGACATACCCATCTGTCGCGGTGACCTCATGTACTTGGGTGAC	5888
Db	5785	ATATTGGATGCCCTGACCAAGACATCTTTGGCGGCAAGGCTAATCCGATCGAGGAGACG	5844
QY	5889	ATCCTCGACGCCCTTACGAAAACATCTTTTGGCGGGAAGGGCAATCCGATAGAGGAGACG	5948
Db	5845	GGTGAATTTGGTGAGATAGCGGCGGACCGGACACCGGAGGCTATGATCCGGTGTCTGTCA	5904
QY	5949	GGTGAGATGGTGAGATACGCGCCGCCCGGATACGGAGGGCTACGAGCCCGCTCTATCA	6008
Db	5905	ACACTGTGGGCCAGCGTGAGGAGTACTGCGCCCAAGCTGTATACAGAAATGCGTGGCG	5960
QY	6009	ACGCTGTGCGCTCAGCGTGAGGAGTACTGCGCCCGGCTTAATCCAGCAGCGCGCGCG	6064

RESULT 8  
ID PCT-0597-24256-2 STANDARD; DNA; UNC; 6315 BP.  
AC xxxxxx  
DT  
Sequence 2, Application PC/TUS9724256  
DE  
Sequence 2, Application PC/TUS9724256  
CC  
GENERAL INFORMATION:  
CC APPLICANT: Cornell Research Foundation, Inc.  
CC TITLE OF INVENTION: INSECT SODIUM CHANNELS FROM  
CC TITLE OF INVENTION: INSECTICIDE-SUSCEPTIBLE AND INSECTICIDE-RESISTANT HOUSE

CC	TITLE OF INVENTION:	FLIES
CC	NUMBER OF SEQUENCES:	19
CC	CORRESPONDENCE ADDRESS:	
CC	ADDRESSEE:	NIXON, HARGRAVE, DEVANS & DOYLE LLP
CC	STREET:	Clinton Square, P.O. Box 1051
CC	CITY:	Rochester
CC	STATE:	New York
CC	COUNTRY:	USA
CC	ZIP:	14603
CC	COMPUTER READABLE FORM:	
CC	MEDIUM TYPE:	Floppy disk
CC	COMPUTER:	IBM PC compatible
CC	OPERATING SYSTEM:	PC-DOS/MS-DOS
CC	SOFTWARE:	PatentIn Release #1.0, Version #1.30
CC	CURRENT APPLICATION DATA:	
CC	APPLICATION NUMBER:	PCT/US97/24256
CC	FILING DATE:	
CC	CLASSIFICATION:	
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER:	US 08/772,512
CC	FILING DATE:	24-DEC-1996
CC	ATTORNEY/AGENT INFORMATION:	
CC	NAME:	Goldman, Michael L.
CC	REGISTRATION NUMBER:	30,727
CC	REFERENCE/DOCKET NUMBER:	19603/602
CC	TELECOMMUNICATION INFORMATION:	
CC	TELEPHONE:	716-263-1304
CC	TELEFAX:	716-263-1600
CC	INFORMATION FOR SEQ ID NO:	2:
CC	SEQUENCE CHARACTERISTICS:	
CC	LENGTH:	6315 base pairs
CC	TYPE:	nucleic acid
CC	STRANDEDNESS:	singl e
CC	TOPOLOGY:	linear
CC	MOLECULE TYPE:	cDNA
SQ	SEQUENCE	6315 BP; 1711 A; 1344 C; 1595 G; 1665 T; 0 OTHER..
Query Match               56.38; Score 3664; DB 1; Length 6315;		
Best Local Similarity 84.8%; Pred. No. 0.00e+00;		
Matches 4980; Conservative 0; Mismatches 812; Indels 84; Gaps		
Db	151	ATACGATATGATCAGAGGACGAAGATGAAGTCCACAGCGGATCCCACACTTTGAACAG 210
Qy	207	ATCGGATATGATCAGCAGGACGAGGATGAAGTTCACACCGGATCCTACACTTGAACAG 266
Db	211	GGTGTCCTATACCTGTTCGAATGCAGGCGAGCTTCCCGCCGGAATTGCCCTCCACTCT 270
Qy	267	GGTGTGCAATACTGTTTCGATTGCAGGCGAGCTTCCCGCGGAAATTGCCCTCCACTCT 326
Db	271	CTCGAGGATATCGATCCCTTCTACAGTAATGTACTCACATTTGTAGTATAAGTAAAGA 330
Qy	327	CTCGAGGATATCGATCCCTACTACACAATGTACTGACATTCGTAGTTGTAAGCAAAGA 386
Db	331	AAGGATATTTTTTGGTTTTTCTGCTCAAAAGCAATGTGGCTGCTCATCCATTCAATCCG 390
Qy	387	AAAGATATTTTTCGCTTTTCGATCAAAAGCAATGTGGATGCTCATCCATTCAATCCG 446
Db	391	ATACGTCGTAGTGCATTTATATTTTAGTGCATCCCTGTTGTTTGGTATTCAATATCAC 450
Qy	447	ATACGTCGTGTGGCATTTTACATTTAGTGCATCCATATATTTTCCCTATTTCATCATC 506
Db	451	ACTATTCTAACTAATGTATTTTAAATGATAATGCCGACACGCCACGGTCGAATCCACA 510
Qy	507	ACAATTCCTGCTCAACTGCATCCCTGATGATGAATCCGACACGCCACGGTTAGTCCACT 566
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Qy	567	GAGGTGATATTCACCGGAATCTTACACATTTGAATCAGCTGTTAAAGTGATGGCACCAG 626
Db	571	TTCAATTTATGCCGTTTACGTATCTTAGAGATGCATGGAATTTGGCTGGACTTCGTAGTA 630
Qy	627	TTCAATTTATGCCGTTTACGTATCTTAGAGATGCATGGAATTTGGCTGGACTTCGTAGTA 686

Dbb 631 ATAGCTTTAGCTTATGTGACCATGGGCATAGATTTAGTGAATCTCGCAGCTTTGAGAACAA 690  
QY 687 ATAGCTTTAGCTTATGTGACCATGGGTATAGATTTAGTGAATCTAGCAGCTTCGCAAGC 746  
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QY 867 CTGTGCGTGTTCGCGTGTATGGCCCTACAGATCTATATGGCGTCTCACCGAGAAGTGC 926  
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QY 1107 CGAATCCGAATTTGGCTTACACAGCTTCGATTTGCTCGGATGGCTTCTGTCCGCG 1166  
Dbb 1111 TTTCTGCTCTACGCCAAGATTTCTGGAGGATCTGTATFACGACGTGTGTCGAAGCAGCT 1170  
QY 1167 TTTCCGCTCATGACACAGGACTTCTGGAGGATCTGTACACAGCTGGTGTGCGCGCGCC 1226  
Dbb 1171 GGACCTGGCAGATGTTGTTCTTTATAGTCATCATCTTCTAGGTTCATCTATCTTGTG 1230  
QY 1227 GGACCATGGCAGATGTTGTTCTTTATAGTCATCATCTTCTAGGTTCATCTATCTTGTG 1286  
Dbb 1231 AATTTTCATTTGGCCATTTGTCATGCTTTATGAGCAATTCGAAAGAGGCCGAAGAA 1290  
QY 1287 AATTTTCATTTGGCCATTTGTCATGCTGTATGAGCAATTCGAAAGAGGCCGAAGAA 1346  
Dbb 1291 GAAGAGGCTGCCGAGGAGGAGCGATCCGAGAGCTGGAAGAGCGGACGACGCGCAAGCG 1350  
QY 1347 GAAGAGGCTGCCGAGGAGGAGCGATACGTGAAGCGGAAGAGCTGCCCGCCGCAAGCG 1406  
Dbb 1351 GCCAACTGGAGAGCGGCGCAATGTAGCAGCTCAAGCGGCTCAGGATCGAGGATGCC 1410  
QY 1407 GCCAAGCTGGAGAGCGGCGCAATGGCAGGCTCAGGCAAGCGGATCGGCTGCCGCG 1466  
Dbb 1411 GCTGCGGCACTGTCATCCGAGATGGCAAGAGTCCCAAGTCTCTTTCATCTAGCTAT 1470  
QY 1467 GAAGAGGCTGCATGTCATCCGGAATGGCCAGAGTCCGACGATTTCTTGATCAGCTAT 1526  
Dbb 1471 GAAGCTGTTGTCGCGGAGAGGCAACGATGACAAACAAAGAGAGATGTGATA 1530  
QY 1527 GAGCTATTTGTCGCGGAGAGGCAACGATGACAAACAAAGAGAGATGTCCATT 1586  
Dbb 1531 CGCAGCGTGAAGTGGNATCGGAGTGGGTGAGCGTTATACAAGACAACCGACCTACC 1590  
QY 1587 CGGAGGCTGAGGTGGAGTGGGAGTGGGTGAGCGTTATACAAGACAACCGACCTACC 1646  
Dbb 1591 ACAGCAC-CC--GCTACTAAAGTCCGTAAGTTAGCAGCAGCTTCTTATCTTACCTGCT 1647  
QY 1647 ACAGCACCAAGCTACCAAGTTCTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1706  
Dbb 1648 TCACCAATTTAACCTACCGCGGGGATCAGCTAGTGTTCACAAAGTACACATACGAATGGG 1707  
QY 1707 TCACCGTTTAAACATACGCGAGGATCAGCTAGTGTTCACAAAGTACACATACGAATGGG 1766  
Dbb 1708 CGTGGAGCTTTTGGTATACCAAGTAGGATCGCAAGCCATTTGGTACTGCAACATATCAG 1767

QY 1767 CGTGGCGCTTTTGGTATACCCGTAGCGATCGTAAGCCATTTGGTATTTGCAACATATCAG 1826  
Dbb 1768 GATGCCCAGCAGCATTTGGCCCTATGCGGATGACTCGAATGCCCTAAACCAATGTCGGAA 1827  
QY 1827 GATGCCCAGCAGCAGCATTTGGCCCTATGCGGAGCTCGAATGCCCTACCCGATGTCGGAA 1886  
Dbb 1828 GAGAATGGTCCCATTTAGTATGACAGCCTACTATTGTAATTTAGGTTCTAGACATTTCTCA 1887  
QY 1887 GAGAATGGGCCATCATAGTGGCGTGTACTATGGCAATCTAGGCTCCCGACACATCAG 1946  
Dbb 1888 TATACCTCGCATCAATCAAGAATCTCGTATACATCACATGGTGTATTTATTTGGTGGCATG 1947  
QY 1947 TATACCTCGCATCAGTCCGAATCTCGTATACCTCATCTACATGGCATCTACTCGCGCATG 2006  
Dbb 1948 GCGGCCATGGTGCAGCACAATGACCAAGAGAGCAAAATGGCAGTCCCAACACACGC 2007  
QY 2007 GCGGTATGGCGCTCAGCACAATGACCAAGAGAGCAAAATGGCAGTCCCAACACACGC 2066  
Dbb 2008 AATCAATCAATCGGTGCTGCAACCAATGTTGGCAGTGTACGGCCGGTGTGGCTATGCC 2067  
QY 2067 AATCAATCAGT-GG-GC-GCCACCAATGGCGGACCAC--CTGTC--TGGA--C-A--CC 2114  
Dbb 2068 GATGCCAATCACAGGAAACAAGGATTTAAATGGTTCAGGATTTATACAGACGAAGCT 2127  
QY 2115 AATCACAAGCTC---GATCATCGCGACTAGCAAAATGGCCTGGAGTGCAGCGGACGAAGCT 2171  
Dbb 2128 GGCAAAATAAACCACACGCAATCTTTTATCGAGCCCGTCCAAACTCAACACAGTGGTA 2187  
QY 2172 GGCAAGATTAACATCATGACAAATCTTTTATCGAGCCCGTCCAGACACAACGCTGTT 2231  
Dbb 2188 GACATGAAGATGTTATGGTCTTAAATGTATCATTTGAACAAGCCGCTGGTTCGCGCATG 2247  
QY 2232 GATATGAAGATGTGTGCTGCTGAATGATCATCATCAACAGCCGCTGGTTCGCGACAGT 2291  
Dbb 2248 CGTCTAGTGAACAGGTG-----AGGACGATGACGAAGAT 2283  
QY 2292 CGGCAACGAGTACGCGGTGCTCCTGTTTACTATTTCCTCAACAGGAGCATGACGAGAT 2351  
Dbb 2284 GGTCCCACTTCAAGGACATCGCCCTCGAATATATCTTAAAGGCATCGAAATCTTTGT 2343  
QY 2352 GGGCGGAGTTCAAGACAGGCACTCGAAGTATCTCAAGGCACTGATGTTGT 2411  
Dbb 2344 GTATGGGACTGTTGTTGGTGTGTTAAATTTTCAGAAATGGGTCTCCTTTATTTGTTTC 2403  
QY 2412 GTGTGGGACTGTTGCTGGGTTTGGTTGAAATTTTCAGAGTGGGTATCGCTCATCTCTC 2471  
Dbb 2404 GATCATTTCTGGAGCTCTTTCATACCTGTGTTATTTGGTCAATAACAATGTTCTATGCC 2463  
QY 2472 GATCCTTCGTCGAGCTCTTCATCAGCTGTGCAATTTGGTCAACACAGATGTTCTATGGCA 2531  
Dbb 2464 ATGGATCATCACGACATGAATCCGGAATTTGGAGAAGTGTCTGAAAGTGTGAATTTTC 2523  
QY 2532 ATGGATCACACGATATGAACAAGAGATGGAACGCGTGTCTCAAGAGTGGCAACTATTTTC 2591  
Dbb 2524 TTCAGGCGCACTTTTGAATTTGAGCCAGCATGAACACTGATGGCCATGAGCCCCAAGTAC 2583  
QY 2592 TTCAGGCGCACTTTGCAATCGAGGCCACCATGAAGCTAATGGCCATGAGCCCCAAGTAC 2651  
Dbb 2584 TACTTCCAGGAAGGCTGGAACATTTTCGATTTTCAATTTATTTGGGCTGTCTCTCTGGAA 2643  
QY 2652 TATTTCCAGGAGGCTGGAACATCTTCGACTTCATTTATCGTGGCCCTATTCCTATTTG 2711  
Dbb 2644 TTGGGCTGGAGGTTCCAGGGCTGTGCGGTGTGTGAGAAGTGTTCGTTTCGTTTCGTTGTA 2703  
QY 2712 CTGGGACTCGAGGTTGTCAGGGTCTGCGGTATTTGCGTTCCTTTTCGATTTCTGCTGTA 2771  
Dbb 2704 TTCAATTTGGCAAAATCATGCCCCACACTGAATTTACTCATTTTCGATTTATGGCCGGA 2763  
QY 2772 TTCAAACTGGCCAGTCTTGGCCCCACACTTAATTTACTCATTTTCGATTTATGGGACG 2831  
Dbb 2764 ATGGGTGATTTGGGTAATCTGACATTTTGTACTTTGCAATTTATCATCTTTCGCGCTG 2823









QY 2712 CTGGGACTCGAGGTGTCCAGGCTCTCGTATTGCGTTCTTTTCGATTGCTGCGTGA 2771  
Db 2704 TTCAAAATGGCAAAATCATGCGCCACACATGAATTTACTATTTCGATTATGGCCGAGCA 2763  
QY 2772 TTCAAACTGGCCAAAGTCTTGGCCACACATTAATTTACTCATTTTCGATTATGGACGACC 2831  
Db 2764 ATGGGTGCATTGGGTAAATCTGACATTTGTACTTTGGCAATATCATCTTCATCTTTGGCCGTG 2823  
QY 2832 ATGGCGCTTTGGGTAACTGACATTTGTACTTTGCAATATCATCTTCATCTTTGGCGTG 2891  
Db 2824 ATGGGAATGCAACTTTTCGGAAGAAGACTATATTGACACAAAGATCGCTTCAAGGACCAAT 2883  
QY 2892 ATGGGAATGCAACTTTTCGGAAGAAGATTTATCATGATCACAAGACCGCTTTTCGCGATGCG 2951  
Db 2884 GAATTACCGCGCTGGAAATTTACCGGACTTCATCGACAGCTTCATGATGTTCCGAGTG 2943  
QY 2952 GACCTGCGCGCTGGAACTTTACCGGACTTTATGCACAGCTTCATGATCGTTCCGGGTG 3011  
Db 2944 CTGTGCGGAGAGTGGATCGAGTCCATGTGGGACTGCTATGTGTGGCGGATGTCAGCTGT 3003  
QY 3012 CTCTGCGGAGAAATGGATCGAGTCCATGTGGGACTGCTATGTGTGGCGGATGTCGTCG 3071  
Db 3004 ATACCCCTCTTTTGGCCAGGCTGCTGATCGGCAATTTTGTGTGTTCTTAATCTTTTCTTA 3063  
QY 3072 ATTCCTCTCTTTTGGCCAGCGTTGTATCGGCAATCTTGTGTACTTAACCTTTTCTTA 3131  
Db 3064 GCTTTGCTTTTGTCCAACTTTCGTTTCATCTAGTTTATCAGCCCGGACTGCGGCAATGAT 3123  
QY 3132 GCTTTGCTTTTGTCCAAATTTTGGCTCATCTAGCTTATCAGCGCGGACTGCGGATACGAT 3191  
Db 3124 ACCAATAAATPAGCAGAGCCCTTCAATCTGATTGCTCGTTTAAAGAACTGGGTGAACGCT 3183  
QY 3192 ACGAATAAATAGCGAGGCTTCAATCGAATTTGGCCGATTTAAAGCTTGGGTAAAGCT 3251  
Db 3184 AATATTGCGGATTTGTTTAACTTAACTGAAATTAATTAAGAACTCAAAATAGTGACAA 3243  
QY 3252 AATATTGCTGATTTTCAAGTTAATACGTAAACAAATTTGACAAATCAAAATAGTGATCA 3311  
Db 3244 CCATCAG-----A-CA-----TGG--CGAT-A--ATG----- 3265  
QY 3312 CCATCAGGTGAGAGGACCAACCATCAGTTGGATTTTGGAGCGNAGACATGTTGACAAC 3371  
Db 3266 -AATCGGATTTGGCTATGACGAATCATGGCGGATGGCTTGATCAAAAAGGATGATGAAG 3324  
QY 3372 GAATCGGAGCTGGCCAGCAGAGATCCTCGCCAGCGCTCATCAAGAAGGGGATCAAG 3431  
Db 3325 GCGCAGACCCAGCTGGAGGTGGCCATTGGCGATGGCATGGATTCAGCATACATGGCGAT 3384  
QY 3432 GAGCAGACGCACTGGAGGTGGCCATCGGGATCGGATGGAAATTCAGCATACAGCGCGAC 3491  
Db 3385 ATGAAAAACAACAGCCCAAGAAATCAAAATTCATAACACACACAGCATGATTGGAAC 3444  
QY 3492 ATGAAGACACACAGCCGAGAAATCCAAATATCTAAATACGCAACGATGATTGGCAAC 3551  
Db 3445 TCAATAAACCAACCAAGACAATAGACTGGAACATAGAGCTAAACCATAGAGTTTGTCCATA 3504  
QY 3552 TCAATTAACCAACCAAGACAATAGACTGGAACACAGAGCTAAACCATAGAGTTTGTCCATA 3611  
Db 3505 CAGGAGATGACACTGCCAGCATTAACCTCATATGTTAGCCATAAGATTCGACCAATTCAAG 3564  
QY 3612 CAGGACGACGACACTGCCAGCATTAACCTCATATGTTAGCCATAAGATTCGACCAATTCAAG 3671  
Db 3565 GACGAGACCCACAAGGGCAGCGCCGAGACCATCGAGGGCGAGGAGAGAACGCGCTCAGC 3624  
QY 3672 GACGAGACCCACAAGGGCAGCGCCGAGACCATCGAGGGCGAGGAGAGAACGCGCGCAGC 3731  
Db 3625 AAGAGGACCTCGGCTCGACGAGGAATCGACGAGGAGGCGCGAGGGCGATGAGGGCCAG 3684  
QY 3732 AAGGAGGATTTAGGTCTCGACGAGGAATCGACGAGGAGGCGGAATGCGAGGAGGGCCCG 3791  
Db 3685 CTGGATGTTGATCATCATCTATCCCAAAACGACGAGATAATCGACGACTATTCGG 3744  
QY 3792 CTCGACGGTGATATCATTTATTCATGCACA---CGACGAGGATATCTCGATGAATATCCA 3848

Db 3745 GCCGACTGTTCCCGACTCGTACTACTACAAGTATTCGGATCTTTGGCGGCGACGAGAC 3804  
QY 3849 GCTGATTCTGCCCGATTCTGTAATAAGAAATTCGGATCTTTAGCGGGTGACGATGAC 3908  
Db 3805 TCGCCGTTCTGGCAAGGATGGGCAATTTAGACTGAAAACCTTTTCAATTAATTAATAAT 3864  
QY 3909 TCGCCGTTCTGGCAAGGATGGGCAATTTAGACTGAAAACCTTTTCAATTAATTAATAAT 3968  
Db 3865 AAATATTTTGAACCGCAGTTATCATTATGATTTTAAATGAGTACTAGCTTTGGCCCTTA 3924  
QY 3969 AAATATTTTGAACCGCAGTTATCATTATGATTTTAAATGAGTACTAGCTTTGGCAATTA 4028  
Db 3925 GAAAGATGTTTCAATTTACCGGATCGACCTCATGAGGAGATATATCTACTATACATGACAGG 3984  
QY 4029 GAAAGATGATACCTGCCACAAGACCCATCTGCAAGGATATTTATATCTATATGACAGA 4088  
Db 3985 ATATTACGGTGATATCTTTTGGAGATGTTGATCAAAATGGTTGGCCCTGGGCTTTAAG 4044  
QY 4089 ATATTACGGTTATATCTTCTTGGAAATGTTAATCAAGTGGTTGGCGCTGGCTTCAA 4148  
Db 4045 GTCTACTTCACAATGCGCTGGTGGCTGATTCGATTCGATTCATCTATCGCTTATA 4104  
QY 4149 GTGTACTTCAACAACGCGTGGTGGCTCGATTTCTGTGATGTCATGATATGCTGTTATC 4208  
Db 4105 AATTTGGTTGCGGTTTGGTTCGGGCTTAAATGATATAGATGATGATCAATGCGCACA 4164  
QY 4209 AACTTCGTTGCTTCACTTGTGGAGCTGGTGTATTAAGCCTTCAAGACTATGCGAAGC 4268  
Db 4165 CTGCGGCGCTTAAGGCAATGGCTGCTCTCTAGATGGGAGGATATGAAGTGTCTGCG 4224  
QY 4269 TTAAGAGCACTGAGACCACTAGCTGCCATGTCCCCTATGTCAGGGCATGAGGCTCGCTT 4328  
Db 4225 AATGGCTGGTTCAAGCTATACCGTCCATCTTCAATGCTTATGCTGCTGCTGATATTT 4284  
QY 4329 AATGGCTGGTACAGCTATACCGTCCATCTTCAATGCTTATGCTGCTGCTATATTT 4388  
Db 4285 TGGCTATTTTGGCCATATATGGAGTACAGCTTTTGGTGGAAATATTTTAAAGTGTAAA 4344  
QY 4389 TGGCTAAATTTTGGCCATATATGGTGTACAGCTTTTGGTGGAAATATTTTAAAGTGGAG 4448  
Db 4345 GATGGTATGACACTGCTGAGCCATGAATCATACCGAATCGTAATGCCCTGCAAAAGT 4404  
QY 4449 GACATGAATGGCAAGAGCTCAGCCAGGATCATACCAATCGCAATCGCTTGGCAGAGC 4508  
Db 4405 GAAACTACACCTGGGAAATTCGCAATGAACTTCGATCATGATAGGTAATCGCTATCTC 4464  
QY 4509 GAGAATACAGTGGTGAATTCAGCAATGAATTCGATCATGATGTAACCGTATCTG 4568  
Db 4465 TGTCTATTTCAAGTGGCCACCTTTAAAGGCTGGATCCAGATTTAGAGCATGCCATTTGAT 4524  
QY 4569 TGGCTTTTCCAAGTGGCCACCTTCAAAAGCTGGATACAAATCATGAACGATGCTATCGAT 4628  
Db 4525 TCACGAGAGGTGGACAGCAGCGGATCCGAGAAACCAATATCTACATGATTTATATTTTC 4584  
QY 4629 TCACGAGAGGTGGACAGCAACCAATTCGTGAACGAGCAATCTACATGATTTATATTTTC 4688  
Db 4585 GTATTCCTTCAATATTTTGGATCATTTTTCACACTCAATCTGTTGCTGGTGTATCATTT 4644  
QY 4689 GTATTCCTTCAATATTTTGGATCCITTTTCACACTCAATCTGTTGCTGGTGTATCATTT 4748  
Db 4645 GATAATTTTAAAGCAAAAGAAAGCAGGTGGATCATTTAGAAATGTTTCATGACAGAA 4704  
QY 4749 GATAATTTTAAAGCAAAAGAAAGCAGGTGGATCATTTAGAAATGTTTCATGACAGAA 4808  
Db 4705 GATCAAAAAGTACTATATGCTGATAAAAGATGGGCTTAAAAAACCATTTAAAGCC 4764  
QY 4809 GATCAAAAAGTACTATATGCTGATAAAAGATGGGCTTAAAAAACCATTTAAAGCC 4868  
Db 4765 ATTCCAAGACCGAGGTGGGACCAAGCAATAGTAGTTTCCAAATAGTTACAGATAAAAA 4824  
QY 4869 ATTCCAAGACCGAGGTGGGACCAAGCAATAGTAGTTTCCAAATAGTTACCGATAAGAAA 4928



Qy	387	AAAGATATTTTTCGCTTTTCGATCAAAAGCAATGTGGATGCTCGATCCATCAATCCG	446
Db	391	ATAGCTCGTGTAGCCATTTATATTTTAGTGCATCCCTTGTTTTCGTTATTCATTATCACC	450
Qy	447	ATAGTCTGTGGCCATTTACATCTTAGTGCATCAATATTTTCCCTATTCATCATCACC	506
Db	451	ACTATTCCTAACTAATTTGTTATTTAAATGATAATGCCGACAACGCCACGGTCGAATCCACA	510
Qy	507	ACAAATTCCTCAACTGCATCCTGATGATAATGCCGACAACGCCACCGTTGAGTCCACT	566
Db	511	GAGTGATATTCACCGGAATCTACACATTTGAATCAGCTGTTAAAGTATGGCAGAGGT	570
Qy	567	GAGTGATATTCACCGGAATCTACACATTTGAATCAGCTGTTAAAGTATGGCAGAGGT	626
Db	571	TTCAATTTATGCCCGTTTACGTATCTTCAGATGATGGAATTTGGCTGGACTTCGTAGTA	630
Qy	627	TTCAATTTATGCCCGTTTACGTATCTTCAGATGATGGAATTTGGCTGGACTTCGTAGTA	686
Db	631	ATAGCTTTAGCTTATGTGACCATGGGCATAGATTTAGGTAATCTCGCAGCTTTGAGAACA	690
Qy	687	ATAGCTTTAGCTTATGTACCATGGGTATAGATTTAGGTAATCTAGCAGCCCTCGGAACG	746
Db	691	TTTAGGCTACTCGGAGCTCTGAACCCGTAGCCATTTGCCAGTCTAAAAACCATTTCT	750
Qy	747	TTTAGGCTGTGCGAGCGCTTAAACCCGTAGCCATTTGCCAGGCTTGAAGACCATCGTC	806
Db	751	GGTCTGCTCATGAATCTGTAAAAAATCTACGCGATGTGATAATTTTGACAATCTTTTTC	810
Qy	807	GGCCCGCTAATCAATCGGTGAAGAATCTGCCGATGTGATATCTCGACCATTTCTTCC	866
Db	811	CTGTCGGTGTTCGCGCTGATGGCCCTACAAATCTATATGGGTGTCTAAACAAAAAGTGC	870
Qy	867	CTGTCGGTGTTCGCGTGTGATGGCCCTACAGATCTATATGGGCGTCTCACCGAGAAGTGC	926
Db	871	ATTAACAGATTTCCCTTGGACGCGAGTTGGGCAATCTGACCGATGAAATCGTTTCTA	930
Qy	927	ATCAAGAAGTTCCCGCTGGACGGTTCTTGGGCAATCTGACCGACGAGAATCGGACAT	986
Db	931	CACAATAGCAACAGTTTCCAATTTGGTTTACGGAGAACGATGCGAGTCTATTCGGTGTGC	990
Qy	987	CACAACTCGCAATAGTCCCAATTTGGTATTCGGAGGACGAGGCAATCTCAATTTCCGTTATGC	1046
Db	991	GGGAATCTATCCGGTGTGGGCAATTCGGCGCAAGATTAAGTCTGCGTGCAGGGGTTCCGC	1050
Qy	1047	GGCAATATATCCGGTGTGGGCAATTCGGAGACGATTAAGTCTGCGTGCAGGGGTTTGGT	1106
Db	1051	CCGAATCCCAACTACAGACTACACAGTTTCAGCTCATCTTCCTAGTGGGCTTCCCTGTGGCG	1110
Qy	1107	CCGAATCCGAATTTATGGCTACACAGCTTCGATTCGTTAGTTCGATTCGTTAGTTCGCGC	1166
Db	1111	TTTCGCTCATACCAAGATTTCTGGGAGGATCTATACGACGCTGCTCGACAGAGCT	1170
Qy	1167	TTCCGGCTGATGACACAGGACTTCTGGGAGGATCTGACAGCTGGTGTTCGGCGCGCGC	1226
Db	1171	GGACCTCGGCACATGTTGTTCTTTTAGTCACTATCTTCCTAGTTCATTTATCTTTGTG	1230
Qy	1227	GGACCATGGCACATGCTGTTCTTTTAGTCACTATCTTCCTAGTTCATTTATCTTTGTG	1286
Db	1231	AATTTGATTTTGGCCATGTTGCCATGCTTATGACGAATTTGCAAAAGAGCGCGCAAGAA	1290
Qy	1287	AATTTGATTTTGGCCATGTTGCCATGCTGATGACGAATTTGCAAAAGAGCGCGCAAGAA	1346
Db	1291	GAGAGGCTCCCGAGGAGGCGATCCAGAAAGCTGAAGAGCGGACGACGCAAGCGC	1350
Qy	1347	GAGAGGCTGCCAAGAGGAGGCGATACGTGAAGCGGAAGCTGCGCGCGCGCAAGAGC	1406
Db	1351	GCCAACTGGAGGAGGCGGCAATGTAGCAGCTCAAGCGGCTCAGGATGACAGCGGATGCC	1410
Qy	1407	GCCAAGCTGGAGGAGGCGGCAATGGCAGGCTCAGGACGACGCGGATGCGGCTGCCGC	1466
Db	1411	GCTGGCGAGCTCTGCATCCGAGATGGCAAGAGTCCACGTAATCTTGTGATTAAGTAT	1470

Db	2524	TTCA	GGCCACTTTT	TC	CAATTTGAGG	CCAGCATGA	AAACTGATGG	CCCATGAGCC	CGAAGTAC	2583
Qy	2592	TTCA	CGCCACCTTT	TC	CCATCGAGG	CCACCATTGA	AGCTTAATGG	CCCATGAGC	CCCAAGTAC	2651
Db	2584	TACT	TTCCAGGA	AGCGCTTG	GAACATTTTC	GATTTTCAT	TATTATTGG	CGCTTGCTCTC	GCTCGGAA	2643
Qy	2652	TATTT	CCAGGAGGCT	TG	GAACATCTTC	GACTTCATAT	TCGTGGCCCTAT	C	CGCTATTGGAA	2711
Db	2644	TTGG	CGCTTGAGG	GGTTC	CAGGCGCTG	CGGTGTGTG	AGAAGTTTTC	GTTCGTTGCT	TCGTGTA	2703
Qy	2712	CTGG	ACTCGAGG	GTTC	CAGGCTGT	CCGTTATTC	CGCTTCTT	TCGATTGCT	CGTGTA	2771
Db	2704	TTCA	AATTTGCC	AAATCAT	TGGCCACAC	TGAATTTAC	TTCATTTTC	GATTTAT	TGGCCGGA	2763
Qy	2772	TTCA	AACTGGCC	AAAGTCTT	TGGCCACAC	TAAATTTAC	TTCATTTTC	GATTTAT	TGGACGCA	2831
Db	2764	ATGG	GTGCATTGGG	TAACTCG	ACATTTTG	TACTTTTGC	ATTATCATCTT	CACTCTT	TCGCGTG	2823
Qy	2832	ATGG	CGCTTTGGG	TAACTCG	ACATTTTG	TACTTTTGC	ATTATCATCTT	CACTCTT	TCGCGTG	2891
Db	2824	ATGG	GAATGCA	ACTTTTC	GGAAGA	ACTATATTG	ACCACA	AGGATCGCTT	CAAGGACCAT	2883
Qy	2892	ATGG	GAATGCA	CTGTTC	GGAAGA	ATTATCAT	GATCACA	AGGACCGCTT	CCGATGGC	2951
Db	2884	GAAT	TACCGCGCT	TGAATTT	CACGACTTC	ATGCACAC	AGCTTCAT	GATTTGTT	TCCGAGTG	2943
Qy	2952	GACT	TGCGCGCT	TG	GAACCTTAC	CGGACTTTAT	GCACAGCTTC	ATGATCGT	GTGTCCGGGTG	3011
Db	2944	CTGT	CGGAGAGT	TG	GATCGAGT	CCCATGTGGG	ACTGCATGTAT	GTGGCGGATGT	CAGCTGT	3003
Qy	3012	CTCT	CGGAGAA	TGGATCG	AGTCCATGT	GGGACTGC	ATGTAC	GTGGCGGATGT	CTCTGC	3071
Db	3004	ATAC	CTTCTTTT	TGGC	ACGGTCTG	ATCGGCAATTT	TGTGGTCTTA	ATATTTTCTTA		3063
Qy	3072	ATT	CTCTTCTT	CTTGTG	CCACCGCTGT	GCATCGGCAATCT	GTGGTACTTA	AACTTTTCTTA		3131
Db	3064	GC	TTTGCTTTT	TG	CAACATTC	GGTTCATCTAG	TTTTATCAG	CCCCGACTT	CGCGACAATGAT	3123
Qy	3132	GC	CTTGCTTTT	TG	TGCAAAATTT	TGGCTCATCTAG	CTTATCAG	CGCGGACTT	CGCGATAACGAT	3191
Db	3124	ACCA	ATAAATAG	CAGAGG	CCCTTCA	ATCTGATTTG	CTCGTTTTA	AGAAGCTTGGG	TGGAACGT	3183
Qy	3192	ACGA	ATAAATAG	CCGAGG	CCCTTCA	ATCGAATTTG	CCCGATTTAA	AGTTGGGTTA	AGCGT	3251
Db	3184	AA	TATTC	CGGATTTG	TTTAA	GTGTAATTC	GAAATAAAT	TGACAAATCA	AAATAAGTGACCA	3243
Qy	3252	AA	TATTC	GTGATTTG	TTTCA	AGTTAATAC	GTAAACA	AAATTTGACA	AAATCAAAATGATCAA	3311
Db	3244	CCAT	CA	G-----	A-CA-----	TGG--CGAT-A--	ATG-----			3265
Qy	3312	CCAT	CAGGTGAG	AGGACCA	CCAGATTC	ATG	TGGATTTGG	AGCGAGAGCAT	TGGTGACAAC	3371
Db	3266	-A	ACTGGAGT	TGGGT	CATGAC	GAATATCAT	GGCGCAT	TGGCTTGAT	CAAAAAAGG	3324
Qy	3372	GA	CTGGAGT	TGGCC	CACGAC	GAGATCTCT	CGCCGAG	CCCTCATCA	AGAAGGGGATCA	3431
Db	3325	GGCG	AGACCC	AGCTG	GAGTGG	CCCATTTG	CGGATGG	CGATGGAGTT	TCACGATACAT	3384
Qy	3432	GAG	CACGCA	CACTGG	AGTGG	CGCCAT	TCGGGGAT	CGGATG	GAAATTCACGATAC	3491
Db	3385	ATGA	AAAAACA	CAAGCC	CAAGAAAT	CAAAATTC	ATAAACA	ACAACA	CAAGCATGATTGGAAC	3444
Qy	3492	ATGA	GAACAACA	AGCCGA	GAANAAT	CCAANAAT	CTAANAAT	ACGCNAC	GATTTGGCAAC	3551
Db	3445	TC	ATAAAC	CAACCA	AGACAAT	TAGACTTGG	AAACAT	TAGCTTAA	ACCATAGAGGTTTCTCCATA	3504
Qy	3552	TC	AATTAAC	CAACCA	AGACAAT	TAGACTTGG	AAACAG	AGCTTAA	ACCATAGAGGTTTCTCCATA	3611
Db	3505	CAG	ACGATGAC	ACTG	CCAG	CAATTA	ACTCATAT	TGTTAG	CGATAGAAT	3564
Qy	3612	CAG	ACGACGAC	ACTG	CCAG	CAATTA	ACTCATAT	TGTTAG	CGATAGAAT	3671

Db	3555	GACGAGACCCAAAGGCGACGCCGCGAGACCATCGAGGGCGAGGAGAAACGCGACGTCCAGC	3624
Qy	3672	GACGAGACCCAAAGGCGACGCCGCGAGACCATCGAGGGCGAGGAGAAACGCGACGCCAGC	3731
Db	3672	GACGAGACCCAAAGGCGACGCCGCGAGACCATCGAGGGCGAGGAGAAACGCGACGCCAGC	3731
Db	3672	GACGAGACCCAAAGGCGACGCCGCGAGACCATCGAGGGCGAGGAGAAACGCGACGCCAGC	3731
Qy	3732	AAGGAGGATTTAGGCTCTCGACGAGGAACCTGGACGAGGAGGGCGAATCGGAGGAGGGCGCG	3791
Db	3685	CTGGATGGTGACATCATCTTCATGCCCAAAACGACGACGAGATTAATCGACGACTATTCGG	3744
Qy	3792	CTCGACGGTGATCATCTATTCATGCGACA--CGACGAGGATTAATCGATGAATATCCA	3848
Db	3745	GCCGACTGTTTCCCGGACTCGTACTACAAGAAGTTTCCGATCTTGGCCGCGCAGCAGGAC	3804
Qy	3849	GCTGATTCGTCGCCGATTCGTACTATAAGAATAATTCGATCTTAGCCGGTGACGATGAC	3908
Db	3805	TCGCGCGTTCGGCAAGGATGGGGCAATTTACGACTGMAAACCTTTTCAATTAATGAAAT	3864
Qy	3909	TCGCGCGTTCGGCAAGGATGGGGCAATTTACGACTGMAAACCTTTTCAATTAATGAAAT	3968
Db	3865	AAATATTTTGAACCGCAGTATFACACTATGATTTTAATGAGTAGCTTAGCTTTGGSCCTTA	3924
Qy	3969	AAATATTTTGAACAGCTGTTATCACTATGATTTTAATGAGTAGCTTAGCTTTGGCATTA	4028
Db	3925	GAAAGATGTCATTTACCCGATCGACCTGTCATGCAAGGATATATCTACTACATGACGACG	3984
Qy	4029	GAAAGATGTCATCTGCCACAAAGCCACTATGCAAGGATATTTTACTATATGACACAGA	4088
Db	3985	ATATTTACGGTGATATCTTTTGGAGATGTTGATCAAAATGTTGGCCCTGGGCTTTAAG	4044
Qy	4089	ATATTTACGGTGATATCTTTTGGAGATGTTGATCAAAATGTTGGCCCTGGGCTTTCAA	4148
Db	4045	GTCCTACTCACCAATGCTGGTGTGGCTGGATTTTCGTTGATGTGCTATCGCTTATA	4104
Qy	4149	GTGTACTTCACCAACGCGTGTGTGGCTCGATTCGTTGATGTGCTATCGCTTATC	4208
Db	4105	AATTTGGTGGCGTTGGTGGCGGCTTAAATGATATAGCGCGTGTTFAGATCAATGCGCACA	4164
Qy	4209	AACCTCGTTGCTTCACTTGTGGAGCTGGTGTGTTTAAAGCCCTTCAAGACTATGCGAAGC	4268
Db	4165	CTGCGCGCCCTAAGGCCATTTGCGGTGCTGTCTAGATGGGAGGGTATCAAAAGTTGTCGTG	4224
Qy	4269	TTAAGAGCATGAGACACATACGTGCCATGTCCCCTATGACGGGATGAGGGTGGTGGT	4328
Db	4225	AATCGCTGGTTCAAAGTATACCGTCCATCTTCAATGTGCTATTGGTGTGCTGATATTT	4284
Qy	4329	AATCGCTGGTACAAGCTATACCGTCCATCTTCAATGTGCTATTGGTGTGCTATATTT	4388
Db	4285	TGGCTTATTTTGGCAATATGGGAGTACAGCTTTTGGCTGGAAAAATTTTTAAGTGTAAA	4344
Qy	4389	TGGCTAATTTTGGCAATATGGGGTGTACAGCTTTTGGCTGGAAAAATTTTTAAGTGTGCGAG	4448
Db	4345	GATGGTAATGACACTGTGCTGAGCCATGAATCATACCGAATCGTAATGCCTGCAAAAGT	4404
Qy	4449	GACATGAATGGCAGAAAGCTACGCCACGAGATCATACCAAAATCGCAATGCCTGGCAGAGC	4508
Db	4405	GAAAACTACACTGGGAAAAATTCGGCAATGAACCTTCGATCATGTAGTAATGCGTATCTC	4464
Qy	4509	GAGAACTACACTGGGTTGATTCAGCAATGAATTCGATCATGTAGTAATGCGTATCTC	4568
Db	4465	TGCTATTTCAGTGGCCACCTTTAAGGCGTGGATCCAGATTAATGAACGATGCCATTGAT	4524
Qy	4569	TGCTTTTTCAGTGGCCACCTTTAAGGCGTGGATCCAGATTAATGAACGATGCCATTGAT	4628
Db	4525	TCACGAGGTTGACAGCAGCGATCCGAGAAACCAATATCTACATGTATTTATTTTC	4584
Qy	4629	TCACGAGGTTGACAGCAGCAACCAATTCGTTGAACCAACATCTACATGTATTTATTTTC	4688
Db	4585	GTATCTTCATATTTTGGATCATTTTTTCACACTCAATCTGCTTCATTTGGTGTATCATTT	4644
Qy	4689	GTATCTTCATATTTTGGATCCTTTTTCACACTCAATCTGCTTCATTTGGTGTATCATTT	4748
Db	4645	GATAATTTTATGAACAAAAAGAAAGCAGGTGGATCATTAAGAAATGTTTCATGACAGAA	4704

4749 GATAATTTAATAGCAAAAGAAAAAGCAGGTGGATCATTTAGAAATGTTTCATACAGAA 4808  
4705 GATCAGAAAAGTACTATAATGCTATGAAAAGATGGCTCTAAAAAACCACTTAAAGCC 4764  
4809 GATCAGAAAAGTACTATAATGCTATGAAAAGATGGCTCTAAAAAACCACTTAAAGCC 4868  
4765 ATTCAGAACCGAGGTGGCGACCAACGAATAGTATTGAAAATAGTTTACAGATAAAAAA 4824  
4869 ATTCAGAACCAAGTGGCGACCAACGAATAGTATTGAAAATAGTAAACGATAAGAA 4928  
4825 TTCGATAATAATCATATATGTTTATGCTTAAATGCTTAAACATGTTTACATGACCCCTCGATCG 4884  
4929 TTCGATAATAATCATATATGTTTATGCTTAAATGCTTAAACATGTTTACATGACCCCTCGATCGT 4988  
4885 TACGACGCTCCGAGCGCTACACAAATGCTCTCGACAACTCAATGGGATATTCGTAGTT 4944  
4989 TACGATGCTGGGACGCTATACACGCGTCTAGACTATCAATGCGATATTCGTAGTT 5048  
4945 ATTTTCAGTGGCGAATGCTATTAATAATATTCGCTTTACGATATCACTATTTCAAAGAG 5004  
5049 ATTTTCAGTTCGGAATGCTATTAATAATATTCGCTTTACGATATCACTATTTATTGAG 5108  
5005 CCATGGAATTAATTTAGTAGTAGTGTGCTATTTATCCATCTTAGTCTTGTACTCAGC 5064  
5109 CCATGGAATTAATTTAGTAGTAGTGTGCTATTTATCCATCTTAGTCTTGTACTTACG 5168  
5065 GACATCATTTGAGCAATTTCTGATTCGCGGACACTGCTCGGTGTCGAGAGTGCCAAA 5124  
5169 GATATTTACGGAAGTACTTCGTGCGCGACCTGCTCGGAGTGGTGGTGGCGAAA 5228  
5125 GTGGTGTGTCCTCGCTTTAGTCAAGGTGCAAGGTATCCGACGTTGCTGTTCGCG 5184  
5229 GTGGCGGTGTCCTTCGACTGCTGAAGGAGCGCAAGGCAATTCGACACTGCTCTTCGCG 5288  
5185 TTAGCATGTCGTCGCTGCTGCTTTATCAACATTTGCTGTGCTGCTTCTTGGTGAATTC 5244  
5289 TTGGCCATGTCGCTCGCGCCCTGTTCAACATCTGCTGCTGCTTCTTGGTGAATTC 5348  
5245 ATCTTTGCTATCTTTGGCATGCTCTTCTTCATGATGCTCAAGAGAAAGGCGCAATAAT 5304  
5349 ATCTTTGCCATTTTGGCATGCTCTTCTTCATGATGCTCAAGAGAAAGGCGCAATAAT 5408  
5305 GCTGTGTATTAATTTAAGACATTTGGCCAAAGTATGATATTCGCTGTTTTCAGATGCTACC 5364  
5409 GAGCTCTACAACCTCAAGACCTTTGGCCAGACATGATCCTGCTTCTTCAGATGCTGACG 5468  
5365 TCAGCGGTGGATGGTGTGATGAGCATATCAATGAGGAGATTCGATCCACCC 5424  
5469 TCAGCGGTGGATGGTGTGATGAGCATATCAATGAGGAGATTCGATCCACCC 5528  
5425 GACAAGCAAGGGCTATCCGGCAATTTGGTTACGCGACTGTTGGAATACGTTTCTC 5484  
5529 GACAGGCAAGGGCTATCCGGCAATTTGGTTACGCGACTGTTGGAATACGTTTCTC 5588  
5485 CTTTCATATCTAGTATAAGCTTTTGTAGTATTATATATGATATGATGCTGCTCATCTC 5544  
5589 CTCTCATACCTAGTATAAGCTTTTGTAGTATTATATATGATATGATGCTGCTCATCTC 5648  
5545 GAGAACTATAGCAGCTACGAGGATGTACAGGGGTCTCACCGACGACCATGATGAT 5604  
5649 GAGAACTATAGTCAGCCACCGAGGACGTGCAAGAGGGTCTAACCGACGACCATGAC 5708  
5605 ATGCTACTAGGATTTGGCAACAATTCGATCCGGAGGGTACCCAGTACATAAGATACGAC 5664  
5709 ATGCTACTAGATCTGGCAACAATTCGATCCGGAGGGTACCCAGTACATAAGATGATGAT 5768  
5665 CAGCTGTCGAGTTCCTGACAGTGTGAGAGCCGCCCTGCAGATCCACAAGCGGACACAG 5724  
5769 CAGCTGTCGGAATTCCTGGACGCTACTGAGAGCCGCCCTGCAGATCCACAAGCGGACACAG 5828  
5725 TACAAAATCATATCGATGACATGCGCGATATGTCGGGGGACATGATGATGATGATGATGAT 5784

5829 TACAAGATCATATCGATGGACATACCCATCTGTGCGGGTGACCTCATGTACTGCGTCGAC 5888  
5785 ATATTGGATGCCCTGACCAAGGACTTCTTTGGCGCAAGGTAATCCGATCGAGGAGACG 5844  
5889 ATCTTCGAGCCCTTACGAAAGACTTCTTTGCGGGAAGGCAATCCGATAGAGGAGACG 5948  
5845 GGTGAATTTGGTGTGAGATTCGGGGCGGACCGGACCGGAGGCTATGATCCGTTGTGCTCG 5904  
5949 GGTGAGATTTGGTGTGAGATTCGGGGCGGACCGGAGGCTATGAGGCGGCTCTCATCA 6008  
5905 ACATGTGGCGCCAGCGTGTGAGGAGTACTGCGCAAGCTGATACAGATGCGTGGCG 5960  
6009 ACGTGTGGCGTGTGAGGAGTACTGCGCGCGGCTAATCCAGCACGCGCTGGCG 6064

RESULT 11  
ID US-08-608-618-1 STANDARD; DNA; UNC; 6318 BP.  
AC xxxxxx

Sequence 1, Application US/08608618  
DE Sequence 1, Application US/08608618  
CC GENERAL INFORMATION:  
CC APPLICANT: Soderlund, David M.  
CC APPLICANT: Knipple, Douglas C.  
CC APPLICANT: Ingles, Patricia J.  
CC TITLE OF INVENTION: INSECT SODIUM CHANNELS FROM  
CC TITLE OF INVENTION: INSECTICIDE-SUSCEPTIBLE AND INSECTICIDE-RESISTANT  
CC TITLE OF INVENTION: HOUSE FLIES  
CC NUMBER OF SEQUENCES: 19  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESS: Nixon, Hargrave, Devans & Doyle LLP  
CC STREET: P.O. Box 1051, Clinton Square  
CC CITY: Rochester  
CC STATE: New York  
CC COUNTRY: USA  
CC ZIP: 14603  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: PatentIn Release #1.0, Version #1.30  
CC CURRENT APPLICATION DATA:  
CC FILING DATE: US/08/608,618  
CC CLASSIFICATION: 530  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Timian, Susan J.  
CC REGISTRATION NUMBER: 34,103  
CC REFERENCE/DOCKET NUMBER: 19603/600 (CRF D-1657)  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 716-263-1636  
CC TELEFAX: 716-263-1600  
CC INFORMATION FOR SEQ ID NO: 1:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 6318 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: cDNA  
CC SEQUENCE 6318 BP; 1712 A; 1347 C; 1597 G; 1662 T; 0 OTHER.

Query Match 56.2%; Score 3662; DB 19; Length 6318;  
Best Local Similarity 84.7%; Pred. No. 0.00e+00;  
Matches 4979; Conservative 0; Mismatches 813; Indels 84; Gaps 21;

Db 151 ATACGATATGATGACGAGGACGAAGTCCACAGCGGATCCACACTTGAACAG 210  
Qy 207 ATCCGATATGATGACGAGGACGAGTCCACACCGGATCTTACACTTGAACAG 266  
Db 211 GGTGTGCTATACCTGTTTCGAATGACGGGACGTTCCCGCGGGAATTGGCCTCCACTCCT 270  
Qy 267 GGTGTGCCAATACCTGTTTCGAATGACGGGACGTTCCCGCGGGAATTGGCCTCCACTCCT 326







Db	4585	GTATCTCTCATATATATTTGGATCAATTTTTCACACATCAATCTGTCTCAATTTGGTGTATCATTT	4644
Qy	4689	GTATCTCTTCATCATATTTTGGATCCCTTTTTCACACATCAATCTGTCTCAATTTGGTGTATCATTT	4748
Db	4645	GATAATTTTAAATGCAACAAAGAAAGACAGGTGGATCATTTAGAAATGTTTCATGCACAGAA	4704
Qy	4749	GATAATTTTAAATGAGCAAAAGAAAAGACAGGTGGATCATTTAGAAATGTTTCAATGCACAGAA	4808
Db	4705	GATCAGAAAAGTACTATATGCTATGAAAAGATGGGCTCTAAAAAACCAATTTAAAAGCC	4764
Qy	4809	GATCAGAAAAGTACTATATGCTATGAAAAGATGGGCTCTAAAAAACCAATTTAAAAGCC	4868
Db	4765	ATTCCAAGACCCGAGGTGGCGACACAAAGCAATAGTATTTCGAAAATAGTTACAGATAAAAAA	4824
Qy	4869	ATTCCAAGACCAAGGTGGCGACACAAAGCAATAGTCTTTGAAATAGTAAACCGATAAGAAA	4928
Db	4825	TTCGATATATCATATATGTTTGTTCATCTGGCTTAAACATGTTTACCATGACCCCTCGATCCG	4884
Qy	4929	TTCGATATATCATATATGTTTGTTCATCTGGCTTGAACATGTTTCAACATGACCCCTCGATCCG	4988
Db	4885	TAGCAGCCCTCCGAGGCGTACAACATGTCCTTCGACAAACTCAATGGGATATTCGTAGTT	4944
Qy	4989	TACGATGCGTTCGACACGTTATACGCGGTCTTAGACTATCTCAATGCGATATTCGTAGTT	5048
Db	4945	ATTTTCAGTGGCGAATGTCTATAAAATATTTTCGCTTTACGATATCACTATTTTCAAAAGAG	5004
Qy	5049	ATTTTCAGTTCGCAATGTCTATAAAATATTTTCGCTTTACGATATCACTATTTTATTATGG	5108
Db	5005	CCATGGAATTTATTTTCATCTAGTGTGTCATTTTATCCATCTTAGGTCITGTACTCAGC	5064
Qy	5109	CCATGGAATTTATTTTCATCTAGTGTGTCATTTTATCCATCTTAGGTCITGTACTTATGAC	5168
Db	5065	GACATCATTTGAGAAGTATTTTCGTATCGCCGACACTGCTCCGTTGGTGAGATGGCCAAA	5124
Qy	5169	GATATATTGAGAAGTACTTTCGTTCGCCGACCCCTGCTCCGAGTGGTGGTGGCGAAA	5228
Db	5125	GTGGGTGTGTCCTCGGTTTATGTCAAAGGGTGCCAAAGGATATCCCGAGCTGTGCTTCGCG	5184
Qy	5229	GTGGCGGTGCTCTTCGACTGTTGAAGGGAGCCAAAGGCACTTCGACACTGCTCTTCGCG	5288
Db	5185	TTAGCCATGTGCTGTGCTGCCCTTATTCACATTTGTCTGTTGCTGTCTTGGTGATGTTTC	5244
Qy	5289	TTGGCCATGTGCTGTGCGGCGCTGTTTCAACATCTGCCCTGCTGCTGCTTCCTTGGTCATGTTTC	5348
Db	5245	ATCTTTGCTATCTTTTGGCATGTCTTCTTCATGCAATGTCAAAGAGAGAGGCGGCAATAAT	5304
Qy	5349	ATCTTTGCCATTTTCGGCATGTCGTTCTTCATGCACTGTAAGGAGAGAGGCGGCAATTAAC	5408
Db	5305	GCTGTGTATAATTTTAAACATATTGGCCAAAGTATGATATTGCTGTTTCAGATGCTTACC	5364
Qy	5409	GAGCTGTACAACCTTCAAGACCTTTGGCCAGAGCATGATCTGCTCTTCAGATGTCGACG	5468
Db	5365	TCAGCCGGTTGGATGGTGTGTAGATGCCATTTCAATGAGGAGAGATTTGGATTTCCACCC	5424
Qy	5469	TCAGCCGGTTGGATGGTGTACTGGACGCCATTTCAATGAGGAAGCATGCGGATTTCCACCC	5528
Db	5425	GACAAGCAAAAGGCTATCCGGGCAATTTGGTTTCAGCGACTGTTTGGAAATTAACGTTTCTC	5484
Qy	5529	GACAGGACAAAAGCTATCCGGGCAATTTGGTTTCAGCGACCTGTTGGTAATTAACGTTTCTC	5588
Db	5485	CTTTCATATCTAGTTATAAGCTTTTTTGATAGTATTATAATATGTACATTTGCTCATTTCTC	5544
Qy	5589	CTCTCATACCTAGTTATAAGCTTTTTTGATAGTATTATAATATGTACATTTGCTCATTTCTC	5648
Db	5545	GAGAACTATAGCCAGCTACGGAGGATGTACAGGAGGCTCTCACCGACGACGATTACGAT	5604
Qy	5649	GAGAACTATATAGTCAGGCCACCGAGGACGTTGCAAGAGGCTCTAAACCGACGACGACTACGAC	5708
Db	5605	ATGTACTACGAGATTTTGGCAACAATTTTCGATCCGGAGGCGACCCAGTACATACGCTACGAC	5664
Qy	5709	ATGTACTATGAGATCTGGCAGCAATTCGATCCGGAGGCGACCCAGTACATACGCTATGAT	5768
Db	5665	CAGCTGTCCGAGTTTCTTGGACGCTGTGGAGCGCCGCTGTCAGATCTCCAAAGCCGCAACAG	5724

Qy	5769	CAGCTGTGCCAAATCTCTGGACGCTACTGGAGCCCGCTGCAGATCCACAAACCGACAAG	5828
Db	5725	TACAAATCATATCGATGACATGCCGATATGTCTGGGCGGACATGATCTACTGTGTGGAT	5784
Qy	5829	TACAAGATCATATCGATGACATACCAATCTCTCGCGGTGACCTCATCTACTTGGGTGCAC	5888
Db	5785	ATATTGGATCCCTTGACCAAGGACTTCTTTGGCGCGCAAGGGTAATCCGATCGAGGAGACG	5844
Qy	5889	ATCCTCGACGCCCTTACGAAGACNCTTCTTTGGCGCGAAGGGCAATCCGATAGAGAGACG	5948
Db	5845	GGTGAATTTGGTGAGATAGCGCGGACCGGACCGACACCGAGGATATGATCCGGTGTCTGTCG	5904
Qy	5949	GGTGAGATTGGTGAGATAGCGGCCCGCCGGATACGGAGGGCTACGAGCCCGTCTCATCA	6008
Db	5905	ACACTGTGGCGCCAGCGTGAGGAGTACTCGGCCACAGCTGATACAGAAATGCGTGGCG	5960
Qy	6009	ACGCTGTGGCGTGACGGTGAGGAGTACTCGGCCCGGCTAATCCAGCACGCGCTGGCG	6064
RESULT	12		
ID	US-08-608-618-2	STANDARD; DNA; UNC; 6318 BP.	
AC	xxxxxx		
DT	Sequence 2, Application US/08608618		
DE	Sequence 2, Application US/08608618		
CC	GENERAL INFORMATION:		
CC	APPLICANT: Soderlund, David M.		
CC	APPLICANT: Knipples, Douglas C.		
CC	APPLICANT: Ingles, Patricia J.		
CC	TITLE OF INVENTION: INSECT SODIUM CHANNELS FROM		
CC	TITLE OF INVENTION: INSECTICIDE-SUSCEPTIBLE AND INSECTICIDE-RESISTANT		
CC	TITLE OF INVENTION: HOUSE FLIES		
CC	NUMBER OF SEQUENCES: 19		
CC	CORRESPONDENCE ADDRESS:		
CC	ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP		
CC	STREET: P.O. Box 1051, Clinton Square		
CC	CITY: Rochester		
CC	STATE: New York		
CC	COUNTRY: USA		
CC	ZIP: 14603		
CC	COMPUTER READABLE FORM:		
CC	MEDIUM TYPE: Floppy disk		
CC	COMPUTER: IBM PC compatible		
CC	OPERATING SYSTEM: PC-DOS/MS-DOS		
CC	SOFTWARE: Patent in Release #1.0, Version #1.30		
CC	CURRENT APPLICATION DATA:		
CC	APPLICATION NUMBER: US/08/608,618		
CC	FILING DATE:		
CC	CLASSIFICATION: 530		
CC	ATTORNEY/AGENT INFORMATION:		
CC	NAME: Timian, Susan J.		
CC	REGISTRATION NUMBER: 34,103		
CC	REFERENCE/DOCKET NUMBER: 19603/600 (CRF D-1657)		
CC	TELECOMMUNICATION INFORMATION:		
CC	TELEPHONE: 716-263-1636		
CC	TELEFAX: 716-263-1600		
CC	INFORMATION FOR SEQ ID NO: 2:		
CC	SEQUENCE CHARACTERISTICS:		
CC	LENGTH: 6318 base pairs		
CC	TYPE: nucleic acid		
CC	STRANDEDNESS: single		
CC	TOPOLOGY: linear		
CC	MOLECULE TYPE: cDNA		
SQ	SEQUENCE 6318 BP; 1713 A; 1349 C; 1592 G; 1664 T; 0 OTHER.		
Query Match	56.2%;	Score 3660;	DB 19; Length 6318;
Best Local Similarity	84.7%;	Pred. No. 0.00e+00;	
Matches	4978;	Conservative 0;	Mismatches 814; Indels 84; Gaps 21;
Db	151	ATACGATATGATGACGAGGACGAAGATGAAGTCCACGCGGATCCACACTTTGAACAG	210
Qy	207	ATTCGATATGATGACGAGGACGAGGATGAAGTCCACACGCGGATCTCTACACTTTGAACAG	266

Query Watch 56.2%; Score 3650; DB 19; Length 6318;  
Best Local Similarity 84.7%; Pred. No. 0.006+00;  
Matches 4978; Conservative 0; Mismatches 814; Indels 84; Gaps 21

b 151 ATACGATATGATGACGAGCAGCAAGATGAAGTCCACACGCGGATCCACACTTTGAACAG 210  
207 ATCCGATATGATGACGAGCAGGATGAAGTCCACAAACGCGATCTTACACTTTGAACAG 265  
y



2412 GTGTGGAGCTGTTGCTGGGTTTGGTTGAAATTTTCAGAGTGGGTATCGCTCATCTGCTTC 2471  
2404 GATCCATTGCTGGAGCTCTTTCATTACCTCGTGATTTGGTCAATACATGTTTCATGGCC 2463  
2472 GATPCCCTTGTGCGAGCTCTTCATPACGCTGTGCAATGCTGCTCAACACGATGTTTCATGGCA 2531  
2464 ATGGATCATCACACATGAATCCGAAATAGAGAAGGTGCTGAAAAGTGGTAACTATTTC 2523  
2532 ATGGATCACACAGATATGAAACAGGAGATGGAACGGGTGCTCAAGAGTGGCAACTATTTC 2591  
2524 TTCACGGCCACTTTTTCGAATTGAGGCCAGCATGAAACTGATGCCATGAGCCCGAAGTAC 2583  
2592 TTCACGGCCACTTTGCCATCGAGGCCACCATGAAGCTAATGSCCATGAGCCCAAGTAC 2651  
2584 TACTTCCAGGAAGCTGGAAACATTTTCGATTTTCATATTATTTGGCCCTTGCTCTGCTGGA 2643  
2652 TATTTCCAGGAGGGCTTGGAAACATTTTCGACTTCATATTATCGTGCCCTATCGCTATTGGAA 2711  
2644 TTGGGCTTGGAGGTGCTCCAGGCGCTGCTGGTGTTCGAGAAGTTTTCGTTGCTTCGTGA 2703  
2712 CTGGGACTCGAGGGTGTCCAGGGCTGTCCGTAATTCGCTTCCTTCGATGCTGCGTGA 2771  
2704 TTCAAATTTGGCAAAATCATGGCCACACACTCAATTTACTCATTTTCGATTTATGGSCCGGACA 2763  
2772 TTCAAACTGGCCAACTTTGGCCACACACTTAATTTACTCATTTTCGATTTATGGACCCACC 2831  
2764 ATGGGTGCATTTGGGTAAATCTGACATTTGTACTTTGCAATTCATCATCTTTTTCGCGTG 2823  
2832 ATGGGCGCTTTGGGTAATCTGACATTTGTACTTTGCAATTCATCATCTTTTTCGCGTG 2891  
2824 ATGGGAATGCACTTTTCGGAAGAACTATATTGACCAAGATCGCTTCAAGGACCAT 2883  
2892 ATGGGAATGCACTGTTCGGAAGAAATTTATCATGATCACAAGGACCGCTTTCGCGATGCG 2951  
2884 GAATTAACCGCGCTGGAACCTTCACCGACTTCATGCACAGCTTTCATGATTTGTTCCGAGTG 2943  
2952 GACCTGCCGCGTGGAACTTCACCGACTTATGCACAGCTTCATGATCGTTCCGCGTG 3011  
2944 CTGTGGGAGAGTGGATCGAGTCCATGTGGGACTGCATGTATGTGGGCGATGTCAGCTGT 3003  
3012 CTGTGGGAGAAATGGATCGAGTCCATGTGGGACTGCATGTACGTGGGCGATGTCGTGTC 3071  
3004 ATACCTCTTCTTTCGCCAGCTGCTGATCGGCAACTTGTGTTCTTAACTTTTCTTA 3063  
3072 ATTCCTCTTCTTTCGCCACCGTTGTCATCGGCAACTTGTGTTACTTAACTTTTCTTA 3131  
3064 GCTTTGCTTTTGTCCAACTTCGTTTCATCTAGTTTATCAGCCCGACTGCCGACATGAT 3123  
3132 GCCTTCTTTGTCCAAATTTTGGCTCATCTAGCTTATCAGCGCGACTGCCGATAACGAT 3191  
3124 ACCAATAAATAGCAGAGGCTTTCAACTCGTATTGCTCGTTTTAAGAACTGGGTGAAACGT 3183  
3192 ACGAATAAATAGCCGAGGCTTTCAACTGAAATTTGGCCGATTTAAAGTTGGGTAAAGCT 3251  
3184 AATATTGCCGATGTTTTTAAAGTTAAATTCGAAATAAATGACAAATCAATAAGTGACCAA 3243  
3252 AATATTGCTGATGTTTTTCAAGTTTAAACGTAAACAAATGACAAATCAATAAGTGATCAA 3311  
3244 CCATCAG-----A-A-CA-----TGG--CGAT-A--ATG----- 3265  
3312 CCATCAGTTGAGAGGACCAACAGATCAGTTGGATTTGGAGCGAGCATGTTGACAAAC 3371  
3266 -AACTGGAGTTGGGTGATCAGCAAAATCATGGCGATGGGTTGATCAAAAAGGGTATGAAG 3324  
3372 GAACTGGAGCTGGGCCACGACGAGATCTTCGCGAGCGCTCATCAAGAAAGGGGATCAAG 3431  
3325 GGGGAGACCCAGCTGGAGGTGGCCATTTGGCGATGGCATGAGGTTACGATACATGCGCAT 3384  
3432 GAGCAGACGCAACTGGAGGTGGCCATCGGGATCGGATCGGAATTCACGATACACGCGAC 3491  
3385 ATGAAAACCAACAGCCCAAGAAATCAAAATTCATCAACACACACGATGATTGGAAC 3444

3492 ATCAAGAACAAACAGCCGGAAGAAATCCAAATATCTAAATAACCAACGATGATTGCCAAC 3551  
3445 TCAATAAACCAACCAAGACAATAGACTGGAAACATGAGCTAAACCATAGAGTTTGTCCATA 3504  
3552 TCAATTAACCAACCAAGACAATAGACTGGAAACAGGACTAAACCATAGAGTTTGTCTTA 3611  
3505 CAGGAGGATGACACTGCCAGCATTTACTCATATGTTAGCCATAAGAAATCGACCATTTCAAG 3564  
3612 CAGGAGGACGACTGCCAGCATTTACTCATATGTTAGCCATAAGAAATCGACCATTTCAAG 3671  
3565 GACGAGAGCCCAAGGCGAGCGCCGAGCAATCGAGGGCGAGGAGAAACGCGACGTCAGC 3624  
3672 GACGAGAGCCCAAGGCGAGCGCCGAGAGCATGGAGGGCGAGGAGAAACGCGACCGCAGC 3731  
3625 AAAGAGGACCTCGGCTCGACGAGGAACCTGGACGAGGAGCGGCGGATGAGGGCCAG 3684  
3732 AAGGAGGATTTAGGTCTCGACGAGGAACCTGGACGAGGAGGCGAATCGCAGGAGGCCCG 3791  
3685 CTGGATGGTGACATTTATCATTTCCATCCCAAAACGAGGAGAGATATTCACGACTATCCG 3744  
3792 CTCGACGGTGATTCATTTATTCATGCACA---CGACGAGGATATCTCGATGAATATCCA 3848  
3745 GCCGACTGTTTCCCGACTCTACTACAAAGAGTTTCCGATCTTGCCCGCGACGAGGAC 3804  
3849 GCTGATGCTGCCCGATTCGTACTATAAGAAATTTCCGATCTTAGCCGGTGACGATGAC 3908  
3805 TCGCGCTTCTGGCAAGGATGGGCAATTTACGACTGAAACCTTTTCAATTAATTTGAAAT 3864  
3909 TCGCGCTTCTGGCAAGGATGGGCAATTTACGACTGAAACCTTTTCAATTAATTTGAAAT 3968  
3865 AATATTTTGAACCGCAGTTATCATATGATTTTAAATGAGTAGCTTACGTTTGGCCTTA 3924  
3969 AATATTTTGAACAGCTGTTATCATATGATTTTAAATGAGTAGCTTACGTTTGGCATT 4028  
3925 GAAGATGTTTCAATTTACCGACTGACCTGATCAGGAGATATCTGATCTACATGGACAGG 3984  
4029 GAAGATGATACATCTGCCACAAGAGCCCATCTGAGGAGATATTTATATATATGGACAGA 4088  
3985 ATATTTACGGTGATATTTCTTTTGGAGATGTTGATCAAAATGTTGGCCCTTGGCCTTTAAG 4044  
4089 ATATTTACGGTTATATTTCTTTTGGAAATGTTAAATCAAGTGTGGCTGCTCGCTTCAAA 4148  
4045 GTCTACTTCACCAATGCTGTTGGCTGGATTTGCGTGAATGCTATGCTATGCTGCTTATC 4104  
4149 GTGTACTTCACCAACGCTGGTGGCTGCGATTTGCGTGAATGCTATGCTGCTATGCTTATC 4208  
4105 AATTTGGTTGCGGTTTGGTGGGCTTAAATGATAGCCGTTTATAGATCAATGCCACA 4164  
4209 AACTCTGTTGCTTCACTTTGAGAGTGGTGTATTTCAAGCCTTCAAGACTATGCGAAGC 4268  
4165 CTGCGCGCCTTAAGGCCATTTGGTGTCTCTAGATGGGAGGTATGAAAGTTGCTGTCG 4224  
4269 TTAAGAGACTGAGACCATCTAGTCCCATGTCCTGATCGAGGCAATGAGGTCGCTGTT 4328  
4225 AATGGCTGGTTTCAAGCTATACCGTCCATCTTCAATGTGCTATTTGGTGTGCTGATATTT 4284  
4329 AATGGCTGGTACAAGCTATACCGTCCATCTTCAATGTGCTATTTGGTGTGCTATATTT 4388  
4285 TGGCTTATTTTGGCCATTTATGGGATGACAGCTTTTGGTGGAAATATTTTAAAGTGA 4344  
4389 TGGCTAATTTTGGCCATTTATGGTGTACAGCTTTTGGTGGAAATATTTTAAAGTGGAG 4448  
4345 GATGTTAATGACACTGTGCTGAGCCATGAAATCATACCAATCGTAAATCGCTGCAAACT 4404  
4449 GACATGAATGGCACAGNAGCTCAGCCACGAGATCATACCAATCGCAATGCCCTGCGAGAC 4508  
4405 GAAACTACACCTTGGGAAATTTGGCAATGAACTTCGATCATCTAGGTAAATGCTATCTC 4464  
4509 GAGAACTACACGCTGGTGAATTCAGCAATGAATTCGATCATGTAGGTAAACCGTATCTG 4568  
4465 TGTCTATTTCAAGTGGCCACCTTTAAGGCTGGATCCGAGTATGAACGATGCCATTTGAT 4524  
4569 TGCCTTTTCCAAAGTGGCCACCTTCAAGGCTGGATACAAATCATGAACGATGCTCGAT 4628



```
CC TOPOLOGY: linear
CC MOLECULE TYPE: CDNA
SO SEQUENCE 1237 BP; 310 A; 309 C; 293 G; 325 T; 0 OTHER.

Query Match      7.2%; Score 472; DB 21; Length 1237;
Best Local Similarity 76.6%; Pred. No. 0.00e+00;
Matches 679; Conservative 0; Mismatches 207; Indels 0; Gaps 0;

Db 187 ACAACTGTCCTGGCAAAATATTTCAAGTGGCTGCAGCTCAACACAGAGCTTTGAGCCA 246
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 4415 ACAGCTTTTCTGCAAAATATTTAAGTCGGAGGACATGAATGCACAGAGCTCAGCCA 4474

Db 247 CGAATCATCCAGACCGAATGCGTGATCTTAGAGAACTACACCTGGGAGAACTACCC 306
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 4475 CGAGATCATCAAAATGCTGCGGAGAGCGGAACTACACGTTGGTGAATTCAGC 4534

Db 307 GATGAACCTTTGACCATGTCGGCAAGGCGTATCTCTCGCTGTTCGAAGTGGCCACTTCAA 366
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 4535 ANTGAATTCATCATGTAGTAACGGGTATCTGTGCGCTTTTCCAGTGGCCACTTCAA 4594

Db 367 GGGATGGATCAGATCATGAACAGCGCTATTGATTTCGAGAGAAGTGGGCCGCAACCTAT 426
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Qy 4595 AGGCTGGATCAAAATCATGAACGATGCTATCGATTACGAGAGGTGGACAAGCAACCAAT 4654

Db 427 ACGGAGAGCAACATCTACATGTACCTGTACTTCTGTGTTCTTCATCATATTGTCGTCAAT 486
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Qy 4655 TCGTGAACGAACATCTACATGTATTTATTTCTGTATTTCTTCATCATATTGTCATCCT 4714

Db 487 CTTCACCTCTCAACCTATTTCATCGGTGTGCATCATCGACAACTTTAACGAACAGAAGAA 546
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Qy 4715 TTTACACTCAATCTGTTTCATGTGTTGTTATCATGTATTAATTTATGACAAAGAA 4774

Db 547 AGCCGGCGGACGCTTGAGATGTTTCATGACCTGAGGACCAAGAAATTAATAATGCCAT 606
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Qy 4775 AGCAGTGGATCATTAAGAAATGTTTCATGACAGAGATCAGAAAAGTACTATAATGCTAT 4834

Db 607 GAAGAAATGGGTTCTAAAAACCTTTAAAAGCTATACCCGAGACAGGAAGTGGCGGCCACA 666
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Qy 4835 GAAAGAAGTGGGCTCTAAAAAACCAATTAAGAGCCATTTCAAAGCAAGAGTGGCGGCCACA 4894

Db 667 AGCGATCTGTTCCGATAGTAGTGACGCAAGAAAGTTCGACATGATCATCTGTTGTCAT 726
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Qy 4895 AGCAATAGCTTTGAAATAGTAACGGATAAGAAATTCGATATAATCATATTGTTATTTCAT 4954

Db 727 CGGCTCAACATGTTGACGATGACCTCGATCACTTACCAGAGTCCGAGACCTTCAGCAC 786
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Qy 4955 TGGTCTGAACATGTTCAACATGACCTCGATCGTTACGATCGTCCGACAGTATAAGCG 5014

Db 787 TGTCTCGACTACCTCAACATGATNTTCATCGTGATATTCAGTTTCAGAGTGCCTATTAAA 846
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Qy 5015 GGTCTAGACTATCTCAATGCGGATATTCGTAGTTATTTTCAGTTCCGAATGCTATTAAA 5074

Db 847 AATGTTCCGCTTACGCTACCATTAATCTTTGTCAGCCATGGAATGTTTCGATTTCGTAGT 906
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Qy 5075 AATATTCGCTTTACCATATCACTATTTATTGAGCCATGGAATTTATTGATGTAGTAGT 5134

Db 907 AGTCAATTTCTCAATTTCTAGTTTGGTATTGAGTGATATTATAGAAAAATATTGTTGTC 966
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Qy 5135 TGTCAATTTATCCATCTTAGTCTTGTACTTAGCATATATTTCGAGAGTACTTCGTGTC 5194

Db 967 ACCCAGCTTACTAGGGTGGTAGAGTAGTACGGAAGTTCGGTGTGTTGCGTCTCGTGA 1026
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Qy 5195 GCGGACCCCTGCTCCGAGTGGTGGTGGTGGGAAAGTGGGCGTGCCTTCGACTGGTGAA 5254

Db 1027 GGGTCGGAAGGATTCGCGACGTTATTGTTGCGGCTGGCCACGGCG 1072
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Qy 5255 GGGAGCCCAAGGCGCATTCGGACACTCTCTCTCGCTTGGCCCATGTGCG 5300

Query Match      5.5%; Score 356; DB 23; Length 5977;
Best Local Similarity 65.1%; Pred. No. 0.00e+00;
Matches 899; Conservative 0; Mismatches 471; Indels 12; Gaps 9;

Db 4195 ATCAACTTTGACAATGTCTGGAGCAGGGTACCTGGCCCTTCTTCAAGTGGCAACCTTCAA 4254
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Qy 4536 ATGAATTTGCATCATGTAGGTAAACGCGTAICTGTGCGCTTTTCCAAGTGGCCACTTCAA 4595

Db 4255 GCGTGGATGGACATCATGTATGCGGCTGTAGATTCCGGAAGCCAGAGCAGCCTGAC 4314
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Qy 4596 GCGTGGATACAAATCAAGCATGCTATCGATTCAAGAGGTGGACAAGCAACCAATT 4655

Db 4315 TACGAGGCAACATCTACATGTATCATCTACTTCGTCATCTTCATCATCTTCGGCTCCTTC 4374
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Qy 4656 CGTGAACGAACATCTACATGTATTTATTTATTTCTTCATCATATTTCGATCCTTT 4715

Db 4375 TTCACCTCAACCTGTTTCATCGGTGTATCATCATCGACAACTTCAACCAAGCAAGAAAG 4434
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Qy 4716 TTCACATCAATCTGTTTCATGTTGTTATCATTTATTTATGACCAAGAAAGAA 4775

Db 4435 TTTGAGG--TCAG--GACATCTTCATGACAGAGGAAGAAAGTACTACATGCCATG 4491
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Qy 4776 GCAGTGGATCATTAAGAAATGTTTCATGACAGAAATCAGAAAAGTACTATAATGCTATG 4835

Db 4492 AAAAAGCTGGCTCCAGAGAACCCACAGAGCCCATCCCCGACCTTTGAACAAATCAA 4551
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Qy 4836 AAAAAGATGGGCTCTATAAAACCATTAAAAAGCCATTTCAGAACCAAGGTGGCGACCACA 4895
```

RESULT 14

ID US-09-024-020A-1 STANDARD; DNA; UNC; 5977 BP.

AC xxxxxx

DT







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M P E L H  
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(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.  
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MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Sun Sep 13 00:05:48 1998; MasPar time 10087.83 Seconds  
Tabular output not generated. 1185.989 Million cell updates/sec

Title: >US-08-554-424-7  
Description: (1-6513) from US08554424.seq  
Perfect Score: 6513 1 TCTAGACGTTGGCCGCATAG.....ACGCGAGTATTAGCTCTAGA 6513  
N.A. Sequence: Comp: AGATCTGCAACCGCGTATC.....TGCCTCATATCGAGATCT

Scoring table: TABLE default  
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 532259 seqs, 918475165 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: emb155  
1:em\_ba 2:em\_htg 3:em\_hum1 4:em\_hum2 5:em\_in 6:em\_om  
7:em\_or 8:em\_ov 9:em\_pat 10:em\_pl 11:em\_ro

Database: genbank107  
12:gb\_ba 13:gb\_htg 14:gb\_in 15:gb\_om 16:gb\_ov 17:gb\_pat  
18:gb\_ph 19:gb\_pl 20:gb\_pr1 21:gb\_pr2 22:gb\_ro 23:gb\_st  
24:gb\_sts 25:gb\_sy 26:gb\_un 27:gb\_v1

Statistics: Mean 12.748; Variance 6.375; scale 2.000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match	Length DB ID Description Pred. No.
1	6513	100.0	6513 17 174672 Sequence 7 from patent 0.00e+00
2	6513	100.0	6513 17 125433 Sequence 7 from patent 0.00e+00
3	6513	100.0	6513 17 133685 Sequence 7 from patent 0.00e+00
4	5992	92.0	6883 14 DROSODCHA Musca domestica insect 0.00e+00
5	3676	56.4	6318 14 DROSODCHA Drosophila melanogaste 0.00e+00
6	3676	56.4	6899 14 MDPARA M.domestica insect 0.00e+00
7	3664	56.3	6315 14 MDU38814 Musca domestica insect 0.00e+00
8	1912	29.4	6096 14 EGU73584 Blattella germanica pa 0.00e+00
9	1910	29.3	6096 14 EGU73583 Blattella germanica pa 0.00e+00
10	1592	24.4	2144 14 DVU26343 Drosophila virilis sod 0.00e+00
11	1441	22.1	5068 14 EGU71083 Blattella germanica pa 0.00e+00
12	696	10.7	986 14 U83872 Haematobia irritans pa 0.00e+00
13	694	10.7	986 14 U83874 Haematobia irritans pa 0.00e+00
14	485	7.4	1840 14 DMU26715 Drosophila melanogaste 0.00e+00
15	448	6.9	947 14 U83871 Haematobia irritans pa 0.00e+00

15	446	6.8	947 14 U83873 Haematobia irritans pa 0.00e+00
17	391	6.0	5616 14 SQDNACH Squid sodium channel-m 7.23e-288
18	392	5.7	5352 22 MMU26707 Mus musculus voltage-g 6.77e-272
19	363	5.6	6822 22 RNSCIII Rat mRNA for brain sod 2.43e-264
20	354	5.4	6826 22 RATSCP6A Rattus norvegicus sodi 8.62e-267
21	352	5.4	7545 22 RATSCAL Rat cardiac specific s 4.10e-255
22	342	5.3	6328 20 HUMHBAX Human voltage-gated so 9.79e-247
23	341	5.2	5203 16 FRBSCAS2 Fugu rubripes mRNA for 6.73e-246
24	341	5.2	7823 20 HUMSKMIA Homo sapiens skeletal 1.03e-241
25	336	5.2	8552 22 RATNACHI Rattus norvegicus sodi 1.03e-241
26	336	5.2	8553 22 RNSCPIIR Rat brain mRNA for sod 1.03e-241
27	334	5.1	5523 22 RNT17153 Rattus norvegicus mRNA 4.86e-240
28	334	5.1	6857 22 RATNCHVS Rat skeletal muscle vo 4.86e-240
29	316	4.9	5952 22 RNU79508 Rattus norvegicus volt 5.38e-225
30	316	4.9	6396 14 ACU66915 Aplysia californica so 5.38e-225
31	320	4.9	8398 22 RNSCPIR Rat brain mRNA for sod 2.46e-228
32	320	4.9	8399 22 RATNACHI Rattus norvegicus sodi 2.46e-228
33	320	4.9	8491 20 HUMH11A Human cardiac tetradot 2.46e-228
34	316	4.9	9316 22 AFU000368 Rattus norvegicus volt 5.38e-225
35	313	4.8	3312 14 DMU26714 Drosophila melanogaste 1.72e-222
36	312	4.8	5955 15 OCU35238 Oryctolagus cuniculus 1.17e-221
37	306	4.7	5505 15 ECU25930 Equus caballus skeleta 1.19e-216
38	308	4.7	6371 20 HSVASCAS H.sapiens mRNA for vol 2.55e-218
39	302	4.6	542 14 HIU32390 Haematobia irritans ex 2.56e-213
40	298	4.6	6344 22 RNU53833 Rattus norvegicus sodi 5.50e-210
41	296	4.5	6524 22 RNSNS R.norvegicus mRNA for 2.54e-208
42	296	4.5	6527 9 A58853 Sequence 1 from Patent 2.54e-208
43	296	4.5	6527 9 A58857 Sequence 7 from Patent 2.54e-208
44	296	4.5	7052 9 A58857 Sequence 5 from Patent 2.54e-208
45	284	4.4	6373 22 MMSNS M.musculus mRNA for SN 2.44e-198

ALIGNMENTS

RESULT 1  
LOCUS I74672 6513 bp DNA PAT 23-DEC-1997  
DEFINITION Sequence 7 from patent US 5688917.  
ACCESSION I74672  
NID g3010813  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 6513)  
AUTHORS Arena,J.P., Feng,G., Hall,L.M., Liu,K., Van Der Ploeg,L.H.T., Wang,P. and Warmke,J.W.  
TITLE Process for functional expression of the para cation channel  
JOURNAL Patent: US 5688917-A 7 18-NOV-1997;  
FEATURES  
source Location/Qualifiers  
1..6513  
/organism="unknown"  
BASE COUNT 1681 a 1548 c 1702 g 1582 t  
ORIGIN

Query Match 100.0%; Score 6513; DB 17; Length 6513;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	1	TCTAGACGTTGGCCGCATAGACAATGACAGAGATTCCGACTCGATATCTGAGGAGAAC	60
Db	61	GCAGTTTGTTCGTCCTTTTACCCGCGAATCATTTGGTGCAAAATCGAACACGCGATTGCCG	120
QY	61	GCAGTTTGTTCGTCCTTTTACCCGCGAATCATTTGGTGCAAAATCGAACACGCGATTGCCG	120
Db	121	CTGAACATGAAAGCAGAGAGAGCTGGAAAGAAAGAGAGCCGAGGAGAGGTGCCCGCAT	180
QY	121	CTGAACATGAAAGCAGAGAGAGCTGGAAAGAAAGAGAGCCGAGGAGAGGTGCCCGCAT	180
Db	181	ATGCGTCGCAAGAAAAACAAAAAGAAATCCGATATGATGACGAGGACGAGGATGAAGGTC	240
QY	181	ATGCGTCGCAAGAAAAACAAAAAGAAATCCGATATGATGACGAGGACGAGGATGAAGGTC	240

Db	241	CACAACCGGATCTACACTTGAACAGGGTGTGCCAATACCTGTTCGATTGCAGGCGAGCT	300
QY	241	CACAACCGGATCTACACTTGAACAGGGTGTGCCAATACCTGTTCGATTGCAGGCGAGCT	300
Db	301	TCCCGCGGAAATTGGCTCCACCTCCTCGAGGATATCGATCCCTACTACAGCAATGTAC	360
QY	301	TCCCGCGGAAATTGGCTCCACCTCCTCGAGGATATCGATCCCTACTACAGCAATGTAC	360
Db	361	TGACATTCTGAGTTGAAGCAAGGAAAGATATTTTTCGCTTTTCTGCAATCAAAAGCAA	420
QY	361	TGACATTCTGAGTTGAAGCAAGGAAAGATATTTTTCGCTTTTCTGCAATCAAAAGCAA	420
Db	421	TGTGGATGCTCGATCCCAATCAATCCGATAGCTGTGGCCATTACATTTCTAGTGCATC	480
QY	421	TGTGGATGCTCGATCCCAATCAATCCGATAGCTGTGGCCATTACATTTCTAGTGCATC	480
Db	481	CATTATTTTCCCTATTTCATCATCACCAATTCCTGTCGCTCACTGCTGATGATATGC	540
QY	481	CATTATTTTCCCTATTTCATCATCACCAATTCCTGTCGCTCACTGCTGATGATATGC	540
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QY	541	CGACAACGCCACGGTTGAGTCCACTGAGGTGATATTACCGGGAATCTACACATTTGAAT	600
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QY	601	CAGCTGTTAAAGTGATGSCACGAGGTTTCATTTTATGCCCCGTTTACGTPATCTTAGAGATG	660
Db	661	CATGGAATTGCTGGACTTCGTAGTAATAGCTTTAGCTTATGTGACCATGGGTATAGATT	720
QY	661	CATGGAATTGCTGGACTTCGTAGTAATAGCTTTAGCTTATGTGACCATGGGTATAGATT	720
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QY	901	ATATGGGCGTGTCCACCGAGAAGTGCATCAAGAAAGTTCCCGCTGGACGGTTCCCTGGGGCA	960
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QY	961	ATCTGACCCAGCAAGACTGGGACTATCAANTCGAATAGCTCCCAATTTGGTATCCGAGG	1020
Db	1021	ACGAGGGCATCTCATTTCCGTTATGGGCAATATATCCGGTCCGGGGCAATCGCAGGAGC	1080
QY	1021	ACGAGGGCATCTCATTTCCGTTATGGGCAATATATCCGGTCCGGGGCAATCGCAGGAGC	1080
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QY	1201	TGTACCAGCTGGTGTGGCGGCGCGGACCATTGGCAGCATGCTGTCTTATAGTCATCA	1260
Db	1261	TCCTTCCTAGGTTTCATCTATCTTGTGAATTTGATTTTGGCCATTTGTCATGCTCGTATG	1320
QY	1261	TCCTTCCTAGGTTTCATCTATCTTGTGAATTTGATTTTGGCCATTTGTCATGCTCGTATG	1320

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Db 2461 TCATCGTCTTCGATCCCTTCGTGAGCTCTTTCATCAGCTGTGCAATGTGGTCAACACGA 2520  
QY 2461 TCATCGTCTTCGATCCCTTCGTGAGCTCTTTCATCAGCTGTGCAATGTGGTCAACACGA 2520  
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Db 2641 GCCCAAGTACTATTTCAGGAGGGCTGGAACATCTTTCGACTTCATTATCGTGGCCCTAT 2700  
QY 2641 GCCCAAGTACTATTTCAGGAGGGCTGGAACATCTTTCGACTTCATTATCGTGGCCCTAT 2700  
Db 2701 CGGTATTGGAACGTGGAGCTCGAGGGTGTCCAGGGTCTGCGGTATTTGCGTTCGAT 2760  
QY 2701 CGGTATTGGAACGTGGAGCTCGAGGGTGTCCAGGGTCTGCGGTATTTGCGTTCGAT 2760  
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QY 2761 TCGTGGTGTATTCAACTGGCCAACTCTTGGCTAACTTGACATTTGACTTTTACTCATTTTCGATTA 2820  
Db 2821 TGGGAGCCACCATGGCGCTTTTGGTAACTTGACATTTGACTTTTACTCATTTTCGATTA 2880  
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QY 3001 TGTTCCGGTGTCTCTCGGAGAAATGGATCGAGTCCATGTGGGACTGCATGTAGTGGGG 3060  
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QY 3781 AGGAGGCCGCTCGACGGTGATATCATTTATTCATGTCACACGACGAGGATATCTCGATG 3840  
Db 3841 AATATCCAGCTGATTCCTGCCCGGATTCGTACTATAAGAAATTTCCGATCTTAGCCGGTG 3900  
QY 3841 AATATCCAGCTGATTCCTGCCCGGATTCGTACTATAAGAAATTTCCGATCTTAGCCGGTG 3900  
Db 3901 AGCATGACTCGCGGTTCTGCAAGGATGGGCAATTTACGACTGAAACCTTTTCAATTA 3960  
QY 3901 AGCATGACTCGCGGTTCTGCAAGGATGGGCAATTTACGACTGAAACCTTTTCAATTA 3960  
Db 3961 TTGAAAATAAATATTTTGAACAGCTGTTTATCCTATGATTTTAAATGAGTAGCTTAGCTT 4020  
QY 3961 TTGAAAATAAATATTTTGAACAGCTGTTTATCCTATGATTTTAAATGAGTAGCTTAGCTT 4020  
Db 4021 TGGCATTAAGAGATGATACATCTGCCACAAGACCCATCTGCAGGATATTTTACTATA 4080  
QY 4021 TGGCATTAAGAGATGATACATCTGCCACAAGACCCATCTGCAGGATATTTTACTATA 4080  
Db 4081 TGGACAGAAATTTTACGGTTATATTTCTTGGAAATGTTAATCAAGTGGTGGCGCTCG 4140  
QY 4081 TGGACAGAAATTTTACGGTTATATTTCTTGGAAATGTTAATCAAGTGGTGGCGCTCG 4140  
Db 4141 GGTTCAAAGTGTACTTCAACACGCGTGGTGTGGCTCGATTTGCTGATTTGCTATG 4200  
QY 4141 GGTTCAAAGTGTACTTCAACACGCGTGGTGTGGCTCGATTTGCTGATTTGCTATG 4200  
Db 4201 CGCTTATCAACTTCGTTGCTTCACTTGTGGAGCTGGTGGTATTCAGGCTTCAAGACTA 4260  
QY 4201 CGCTTATCAACTTCGTTGCTTCACTTGTGGAGCTGGTGGTATTCAGGCTTCAAGACTA 4260  
Db 4261 TCGGAACGTTAAGAGCAGTACAGCAGTACGTCAGGCTGCGCATGTCCCGTATGCGAGGCGATGAGG 4320  
QY 4261 TCGGAACGTTAAGAGCAGTACAGCAGTACGTCAGGCTGCGCATGTCCCGTATGCGAGGCGATGAGG 4320  
Db 4321 TCGTCTGTTAATCGCTGTGTACAGCTATACCGTCCATCTTCAATGTGCTATTTGGTGTGTC 4380  
QY 4321 TCGTCTGTTAATCGCTGTGTGTACAGCTATACCGTCCATCTTCAATGTGCTATTTGGTGTGTC 4380  
Db 4381 TAAATATTTTGGCTAATTTTGGCATAAATGGGTGTACAGCTTTTGGTGGAAATATTTTA 4440  
QY 4381 TAAATATTTTGGCTAATTTTGGCATAAATGGGTGTACAGCTTTTGGTGGAAATATTTTA 4440  
Db 4441 AGTGGCAGGACATGAATGCGACGAGCTCAGCCACGAGATCATACCAATCGCAATGSCCT 4500  
QY 4441 AGTGGCAGGACATGAATGCGACGAGCTCAGCCACGAGATCATACCAATCGCAATGSCCT 4500  
Db 4501 GCGAGAGCGAGAACTACAGTGGTGAATTCAGCAATGAATTCGATCATGTAGGTAAAGC 4560  
QY 4501 GCGAGAGCGAGAACTACAGTGGTGAATTCAGCAATGAATTCGATCATGTAGGTAAAGC 4560  
Db 4561 CGTATCTGTGCTTTTCCAAAGTGGCCACCTTCAAAGGCTGGATACAAATCATCAAGCATG 4620  
QY 4561 CGTATCTGTGCTTTTCCAAAGTGGCCACCTTCAAAGGCTGGATACAAATCATCAAGCATG 4620  
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BASE COUNT		1681 a	1548 c	1702 g	1582 t	ORIGIN	
Query Match 100.0%; Score 6513; DB 17; Length 6513;							
Best Local Similarity 100.0%; Pred. No. 0.00e+00;							
Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
Db	1	CTAGAGCTGGCGCATAGACAAATGACAGAAGATCCGACTCGATATCTGAGGAAGAAC	60				
QY	1	CTAGAGCTGGCGCATAGACAAATGACAGAAGATCCGACTCGATATCTGAGGAAGAAC	60				
Db	61	GCAGTTGTTCCGCTTCTTACCGCGAATCAATGTGCAAAATCGACACGATTCGCG	120				
QY	61	GCAGTTGTTCCGCTTCTTACCGCGAATCAATGTGCAAAATCGACACGATTCGCG	120				
Db	121	CTGAACATGAAAGCAGAGAGCTGGAAGAAAGAGAGCGGAGGAGAGTCCCGGAT	180				
QY	121	CTGAACATGAAAGCAGAGAGCTGGAAGAAAGAGAGCGGAGGAGAGTCCCGGAT	180				
Db	181	ATGTCGCAAGAAAACAAAAGAAATCCGATATGATGACGAGGAGGATGAAGTC	240				
QY	181	ATGTCGCAAGAAAACAAAAGAAATCCGATATGATGACGAGGAGGATGAAGTC	240				
Db	241	CACAACCGGATCTACACTTGAACAGGGTGTGCCAATACCTGTCTGATTCGAGGGAGCT	300				
QY	241	CACAACCGGATCTACACTTGAACAGGGTGTGCCAATACCTGTCTGATTCGAGGGAGCT	300				
Db	301	TCCCGCGGAATGGCCCTCCACTCTCGAGGATATCGATCCCTACTACAGCAATGTAC	360				
QY	301	TCCCGCGGAATGGCCCTCCACTCTCGAGGATATCGATCCCTACTACAGCAATGTAC	360				
Db	361	TGACATTCGTAGTTGAAGCAAGGAAAGATATTTTCGCTTTTCGCAATCAAAAGCAA	420				
QY	361	TGACATTCGTAGTTGAAGCAAGGAAAGATATTTTCGCTTTTCGCAATCAAAAGCAA	420				
Db	421	TGTGGATGCTCGATCCATCAATCCGATACGTGCTGCGCCATTTACATTCCTAGTGATC	480				
QY	421	TGTGGATGCTCGATCCATCAATCCGATACGTGCTGCGCCATTTACATTCCTAGTGATC	480				
Db	481	CATTATTTCCCTATTCATCATCACCAATTCCTCGCAACTGCATCCTGATGATATGC	540				
QY	481	CATTATTTCCCTATTCATCATCACCAATTCCTCGCAACTGCATCCTGATGATATGC	540				
Db	541	CGAACGCCCCAGCTTGAGTCCACTGAGTGATATTCACCGGAATCTACACATTTGAAT	600				
QY	541	CGAACGCCCCAGCTTGAGTCCACTGAGTGATATTCACCGGAATCTACACATTTGAAT	600				
Db	601	CAGCTGTTAAGTATGGCAGGAGTTTCATTTATGCCCGTTTACGTATCTTAGAGATG	660				
QY	601	CAGCTGTTAAGTATGGCAGGAGTTTCATTTATGCCCGTTTACGTATCTTAGAGATG	660				
Db	661	CATGGAATGGCTGGACTTCGTAGTAATAGCTTTAGCTTATGTGACCATGGGTATAGATT	720				
QY	661	CATGGAATGGCTGGACTTCGTAGTAATAGCTTTAGCTTATGTGACCATGGGTATAGATT	720				
Db	721	TAGTAATCTAGCAGCCCTCGAACGTTTGGGTGCTGCGAGCGCTTAAACCGTAGCCA	780				
QY	721	TAGTAATCTAGCAGCCCTCGAACGTTTGGGTGCTGCGAGCGCTTAAACCGTAGCCA	780				
Db	781	TTGTGCCAGGCTTGAAGACCATCGTCGGCGCGCTCATCGAATCGGTGAAGAAATCTGCGCG	840				
QY	781	TTGTGCCAGGCTTGAAGACCATCGTCGGCGCGCTCATCGAATCGGTGAAGAAATCTGCGCG	840				
Db	841	ATGTGATTTCCCTGACCATGTCTCCCTGTCGGTGTTCGGTTCATGGGCTACAGATCT	900				
QY	841	ATGTGATTTCCCTGACCATGTCTCCCTGTCGGTGTTCGGTTCATGGGCTACAGATCT	900				
Db	901	ATATGGCGTCTCACCGAAGTGCATCAAGAAATTCCTCGCTGGAGCGTTCTCTGGGCA	960				
QY	901	ATATGGCGTCTCACCGAAGTGCATCAAGAAATTCCTCGCTGGAGCGTTCTCTGGGCA	960				
Db	961	ATCTGACCGAGAACTGGGACTATCACAAATCGCAATAGCTCCAAATTTGGTATTCGAGG	1020				
QY	961	ATCTGACCGAGAACTGGGACTATCACAAATCGCAATAGCTCCAAATTTGGTATTCGAGG	1020				

QY	961	ATCTGACCGAGAACTGGGACTATCACAAATCGCAATAGCTCCAAATTTGGTATTCGAGG	1020				
Db	1021	ACGAGGGCATCTCATTTCCGTTATGCGGCAATATATCCGGTGGGGCAATGCGAGACG	1080				
QY	1021	ACGAGGGCATCTCATTTCCGTTATGCGGCAATATATCCGGTGGGGCAATGCGAGACG	1080				
Db	1081	ATTACGTGCTGCGAGGGTTTGGTCCGAATCCGAATTTATGGCTACACAGCTTCGATT	1140				
QY	1081	ATTACGTGCTGCGAGGGTTTGGTCCGAATCCGAATTTATGGCTACACAGCTTCGATT	1140				
Db	1141	CGTTCGATGGGCTTCTCTCGCTTCCGCTGATGACACAGGACTTCTGGAGATC	1200				
QY	1141	CGTTCGATGGGCTTCTCTCGCTTCCGCTGATGACACAGGACTTCTGGAGATC	1200				
Db	1201	TGTACAGCTGTGTTCGCGCGCGCCGACCATGGCACATGCTGTCTTTATAGTCATCA	1260				
QY	1201	TGTACAGCTGTGTTCGCGCGCGCCGACCATGGCACATGCTGTCTTTATAGTCATCA	1260				
Db	1261	TCCTCCTAGTTTCATTTCTTCTTGTGAAATTTGATTTTGGCCATTTGTCATGCTGATG	1320				
QY	1261	TCCTCCTAGTTTCATTTCTTCTTGTGAAATTTGATTTTGGCCATTTGTCATGCTGATG	1320				
Db	1321	ACGAATTGCAAGGAGCGCGGAGAGAGAGGCTCCGAGAGGAGGCGCATACGTGAAG	1380				
QY	1321	ACGAATTGCAAGGAGCGCGGAGAGAGAGGCTCCGAGAGGAGGCGCATACGTGAAG	1380				
Db	1381	CGGAAGAAGCTGCCCGCGCAAGCTGGAGGAGCGGCAATGCCAGGCTC	1440				
QY	1381	CGGAAGAAGCTGCCCGCGCAAGCTGGAGGAGCGGCAATGCCAGGCTC	1440				
Db	1441	AGGACAGCGGATGGCGTCCGCGGAGAGAGGCTGCATCGCAATCGGAAATGCCAAGA	1500				
QY	1441	AGGACAGCGGATGGCGTCCGCGGAGAGAGGCTGCATCGCAATCGGAAATGCCAAGA	1500				
Db	1501	GTCCGAGCTATTCCTGCATCAGCTATGAGCTATTTGTTGGCGCGAGAGGCAAGATG	1560				
QY	1501	GTCCGAGCTATTCCTGCATCAGCTATGAGCTATTTGTTGGCGCGAGAGGCAAGATG	1560				
Db	1561	ACAACAAGAGAGAGATGTCATTTCGGAGCTCGAGGTGGAGTTCGGTTCGAGCG	1620				
QY	1561	ACAACAAGAGAGAGATGTCATTTCGGAGCTCGAGGTGGAGTTCGGTTCGAGCG	1620				
Db	1621	TTATACAAAGACACACAGCACCTTACCACAGCACACCAAGCTACCAAGTTTCGTAAGTGA	1680				
QY	1621	TTATACAAAGACACACAGCACCTTACCACAGCACACCAAGCTACCAAGTTTCGTAAGTGA	1680				
Db	1681	GCACGACATCTTATCTTACCTGTTTACCCTTTACATACACAGGGGATCAGTAGTT	1740				
QY	1681	GCACGACATCTTATCTTACCTGTTTACCCTTTACATACACAGGGGATCAGTAGTT	1740				
Db	1741	CTCACAAGTACAGATACGGAACGGAGCTGGCGCTTTGGTATACCCGTTAGCGATCGTA	1800				
QY	1741	CTCACAAGTACAGATACGGAACGGAGCTGGCGCTTTGGTATACCCGTTAGCGATCGTA	1800				
Db	1801	AGCCATTGGTATTTCAACATATCAGGATGCCCAGCAGCACTTGCCTATGCCGAGCT	1860				
QY	1801	AGCCATTGGTATTTCAACATATCAGGATGCCCAGCAGCACTTGCCTATGCCGAGCT	1860				
Db	1861	CGAATGCCGTACCCCGATGTCGGAAGAGAAATGGGGCCATCATAGTCCCGTGTACTATG	1920				
QY	1861	CGAATGCCGTACCCCGATGTCGGAAGAGAAATGGGGCCATCATAGTCCCGTGTACTATG	1920				
Db	1921	GCAATCTAGGCTCCGACACTCATCTATACCTCGCATAGTCCCGAAATTCGTATACCT	1980				
QY	1921	GCAATCTAGGCTCCGACACTCATCTATACCTCGCATAGTCCCGAAATTCGTATACCT	1980				
Db	1981	CACATGGGATCTTACCTGGCGGATGGCGCTCATGGCGCTCAGCAAAATGACCAAGGAGA	2040				
QY	1981	CACATGGGATCTTACCTGGCGGATGGCGCTCATGGCGCTCAGCAAAATGACCAAGGAGA	2040				
Db	2041	GCAATTTGGCAACCGCAACACAGCAATCAATAGTGGGCGCCCAATGCGGCA	2100				
QY	2041	GCAATTTGGCAACCGCAACACAGCAATCAATAGTGGGCGCCCAATGCGGCA	2100				

[illegible]

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Db 4321 TCCTCGTTAATGCGCTGGTACAAGCTATACCGPCCATCTTCAATGTCGCTATGCGTGTGTC 4380  
QY 4321 TCCTCGTTAATGCGCTGGTACAAGCTATACCGPCCATCTTCAATGTCGCTATGCGTGTGTC 4380  
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QY 4381 TAATATTTGGCTAAATTTTGGCCATTAATGGGTGTACAGCTTTTGGCTGGAAATATTTTA 4440  
Db 4441 AGTCCGAGGACATGAATGGCACAAGCTCAGCCACGAGATCATACCAATCGCAATGCGCT 4500  
QY 4441 AGTCCGAGGACATGAATGGCACAAGCTCAGCCACGAGATCATACCAATCGCAATGCGCT 4500  
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QY 4501 GCAGAGCGAGAACTACACGTGGGTGAATTCAGCAATGAATTCGATCATGTAGGTAAGC 4560  
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QY 4561 CGTATCTGCGCTTTTCCAAAGTGGCCACCTTCAAAGCTGGATACAAATCATGAACGATG 4620  
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QY 4621 CTATCGATTCACGAGAGTGGACAAGCAACCAATTCGTGAACGAACATCTACATGATT 4680  
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QY 4741 TTATCATTTGATAATTTTAATGACAAAAGAAAAGAGAGTGATGATTAAGAAATGTTC 4800  
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QY 4801 TGACAGAAGATCAGAAAAGTACTAATAGCTATGAAAAGATGGCTCTTAAAACCAT 4860  
Db 4861 TAAAGCCATTCCAAGACCAAGTGGCGACCAAGCAATAGTCTTTGAAATAGTAACCG 4920  
QY 4861 TAAAGCCATTCCAAGACCAAGTGGCGACCAAGCAATAGTCTTTGAAATAGTAACCG 4920  
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QY 5101 TTATTGAGCCATGGAATTTATTTGATGTAGTATTGTCATTTTATCCATCTTAGGCTTG 5160  
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QY 5581 CGTTTCTCCTCTCATACCTAGTTATAAGCTTTTGTATAGTTATTAATATGATGTTG 5640  
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QY 5701 ACTAGCACATGTATGAGATCTGSCAGCAATTCGATCCGGAGGCGACCCAGTACATAC 5760  
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QY 5761 GCTATGATCAGCTGTCCGAATTCCTGGAGCTACTGGAGCCCCCGCTGCAGATCCACAAC 5820  
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QY 5821 CGAACAAGTACAAGATCATATCGATGGACATACCCATCTGTCGCGGTGACCTCATGCT 5880  
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Db 6481 CCCTCAAGATGCACGGAGTATTAGCTTAGA 6513  
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Qy 6481 CCCTCAAGATGCACGGAGTATTAGCTTAGA 6513

RESULT 3  
LOCUS 133685 6513 bp DNA PAT 27-JAN-1997  
DEFINITION Sequence 7 from patent US 5593864.  
ACCESSION 133685  
NID 91824476  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
Arenas,J.P., Peng,G., Hall,L.M., Liu,K., Van Der Ploeg,L.H.T.,  
Wang,P. and Warmke,J.W.  
TITLE Process for functional expression of the para cation channel  
JOURNAL Patent: US 5593864-A 7 14-JAN-1997;  
FEATURES Location/Qualifiers  
1. 6513  
source /organism="unknown"  
BASE COUNT 1681 a 1548 c 1702 g 1582 t  
ORIGIN

Query Match 100.0%; Score 6513; DB 17; Length 6513;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 TCTAGAGTTGGCGGATAGACAATGACAGAAGATCCGACTCGATATCTGAGGAAGAC 60

Db 61 GCAGTTGTTCCGTCCTTTACCCGCGAATCATTTGGTGCATAATCGACACGCAATTCGCCG 120  
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Qy 61 GCAGTTGTTCCGTCCTTTACCCGCGAATCATTTGGTGCATAATCGACACGCAATTCGCCG 120

Db 121 CTGAACATGAAAGCAGAGAGCTGGAAAGAAAGAGAGCGGAGGAGAGTGCCCGAT 180  
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Qy 121 CTGAACATGAAAGCAGAGAGCTGGAAAGAAAGAGAGCGGAGGAGAGTGCCCGAT 180

Db 181 ATGTCGCAAGAAAAACAAAAGAAATCCGATATGATGACGAGGAGAGATGAAGGTC 240  
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Qy 181 ATGTCGCAAGAAAAACAAAAGAAATCCGATATGATGACGAGGAGAGATGAAGGTC 240

Db 241 CACAACGGATCTTACACTTGAACAGGCTGGCCAATACCTGTTCTGATTCAGGGCAGCT 300  
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Qy 241 CACAACGGATCTTACACTTGAACAGGCTGGCCAATACCTGTTCTGATTCAGGGCAGCT 300

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Db 361 TGACATTCGTAGTTGTAAGCAAGAAAGAAATATTTTCGTTTCTGTCATCAAAACAA 420  
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Qy 361 TGACATTCGTAGTTGTAAGCAAGAAAGAAATATTTTCGTTTCTGTCATCAAAACAA 420

Db 421 TGTGGATGCTCGATCCATTAATCCGATACGTCGTGGCCATTTACATTTCTAGTGATC 480  
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Qy 421 TGTGGATGCTCGATCCATTAATCCGATACGTCGTGGCCATTTACATTTCTAGTGATC 480

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Qy 481 CATTAATTTCCCTATTCATCATACACCAATTCGTCGAATCGATCCTGATGATAATGC 540

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Qy 541 CGACACGCCACCGTTGAGTCCACTGAGGTGATATTACCGGGAATCTACACATTTGAAT 600

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Db 661 CATGGAATTTGGCTGGACTTCGTAGTAATAGCTTTAGCTTATGTGACCATGGGTATAGATT 720  
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Qy 661 CATGGAATTTGGCTGGACTTCGTAGTAATAGCTTTAGCTTATGTGACCATGGGTATAGATT 720

Db 721 TAGGTAATCTAGCAGCCCTGCGAACGTTTATAGGTGCTGGAGCGCTTAAACCCGTAGCCA 780  
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Db 901 ATATGGCGTGTCTACCGAAGAGTGCATCAAGAAAGTTCCTCGTGGACGGTTCCTGGGCA 960  
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Qy 901 ATATGGCGTGTCTACCGAAGAGTGCATCAAGAAAGTTCCTCGTGGACGGTTCCTGGGCA 960

Db 961 ATCTGACCGACGAGAACTGGGACTATCAATCGCAATAGCTCCAATTTGATTCGGAG 1020  
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Db 1081 ATACGTGTGCTGACGGGTTTGGTCCGAATCCGAATTTATGGCTACACCACTTCGATT 1140  
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Db 1141 CGTTCCGATGGGCTTTCCTGTCGCTTCGCTGATGACACAGGACTTCTCGGAGGATC 1200  
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Qy 1141 CGTTCCGATGGGCTTTCCTGTCGCTTCGCTGATGACACAGGACTTCTCGGAGGATC 1200

Db 1201 TGTACAGCTGTTGTGCGCGCGCGGACCATGCTGTTCTTTATAGTCATCA 1260  
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Db 1321 ACCAATTGCAAGAGAGCGCGGAGAGAGGCTCCCAAGAGGAGGCGATACGTGAAG 1380  
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Db 1381 CGGAAGAAGCTGCGCGCGCGCAAGCGGCAAGCTGGAGGAGCGGCAATGCGAGGCTC 1440  
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Qy 1381 CGGAAGAAGCTGCGCGCGCGCAAGCGGCAAGCTGGAGGAGCGGCAATGCGAGGCTC 1440

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Db 1501 GTCCGACGATTTCTGATCAGCTATGAGCTATTTTGGCGCGGAGAGGCAAGCATG 1560  
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Qy 1501 GTCCGACGATTTCTGATCAGCTATGAGCTATTTTGGCGCGGAGAGGCAAGCATG 1560

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Qy 1561 ACAACAACAAAGAGAAGATGTCATTCGGAGCGTCCAGGTGGAGTGGGTAGGCGAGG 1620

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Qy 1621 TTATACAAAGACACACGACCTTACCACAGCACACCAAGTTCGTAAGTGA 1680

Db 1681 GCACGACATCTTATCTTACCTTGGTTCACCGTTTAACTATACGAGGGATCATCGTAGTT 1740  
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Qy 1681 GCACGACATCTTATCTTACCTTGGTTCACCGTTTAACTATACGAGGGATCATCGTAGTT 1740

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Qy	1741		
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Db	1801	AGCCATTGGTATTGTCAACATATCAGGATGCCACAGCACTTGCCTATGCGCAGCACT	1860
Qy	1801		
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Db	1861	CGAATGCCGTACCCCGATGTCCGAGAGAATGGGCCCATCATAGTCCCGTGTACTATG	1920
Qy	1861		
		CGAATGCCGTACCCCGATGTCCGAGAGAATGGGCCCATCATAGTCCCGTGTACTATG	1920
Db	1921	GCANTCTAGGCTCCGACACTCATCGTATACCTCCGATCAGTCCGGAATATCGTATACCT	1980
Qy	1921		
		GCANTCTAGGCTCCGACACTCATCGTATACCTCCGATCAGTCCGGAATATCGTATACCT	1980
Db	1981	CACATGGCATCTACTCGCGGCGATGGCGCTCATGGCGCTCAGCACAAATGACCAAGGAGA	2040
Qy	1981		
		CACATGGCATCTACTCGCGGCGATGGCGCTCATGGCGCTCAGCACAAATGACCAAGGAGA	2040
Db	2041	GCAAAATTGCGCAACCCCAACACACAGCAATCAATCACTGGCGGCCACCAATGGCGGCACCA	2100
Qy	2041		
		GCAAAATTGCGCAACCCCAACACAGCAATCAATCACTGGCGGCCACCAATGGCGGCACCA	2100
Db	2101	CCTGCTGGACACCAATCACAGCTCGATCATCGGACTACGAAATGGCGCTGGAGTGCA	2160
Qy	2101		
		CCTGCTGGACACCAATCACAGCTCGATCATCGGACTACGAAATGGCGCTGGAGTGCA	2160
Db	2161	CGGACGAAGCTGCGAAGATTAAACATCATGACAATCCTTTTATCGAGCCCGTCCAGACAC	2220
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		CGGACGAAGCTGCGAAGATTAAACATCATGACAATCCTTTTATCGAGCCCGTCCAGACAC	2220
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Db	2281	GTCGGCACAGTGGGGAAGCGATCGCGGTCTCCGTTTACTATTTCCCAACAGAGGACG	2340
Qy	2281		
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Qy	2341		
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Qy	2401		
		ATGTGTTTTGTGTGGGACTGTGTGGTTGGTTGGAATTTTCAGGAGTGGGTATCGC	2460
Db	2461	TCATCGTCTTCGATCCCTTGGTGGAGCTCTTCATCACGCTGTGCATTTGGTCAACACGA	2520
Qy	2461		
		TCATCGTCTTCGATCCCTTGGTGGAGCTCTTCATCACGCTGTGCATTTGGTCAACACGA	2520
Db	2521	TGTTTCATGGCAATGGATCACCAGATATGAACAAGAGATGGAACGGCTGTCTCAAGAGTG	2580
Qy	2521		
		TGTTTCATGGCAATGGATCACCAGATATGAACAAGAGATGGAACGGCTGTCTCAAGAGTG	2580
Db	2581	GCAACTATTTCTCACCGCCACTTTGGCCATCGAGGCCACCATGAAGCTAATGGCCATGA	2640
Qy	2581		
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Db	2641	GCCCCAAGTACTATTTCCAGGAGGGCTGGAACATCTTCGACTTCATTATCGTGGCCCCAT	2700
Qy	2641		
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Qy	2761		
		TGCTGCGGTATTCAAACTGGCCAACTCTTGCCCCACACTTAATTTACTCATTTTCGATTA	2820
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QY	2821	 TGGAGCGACCATG	GGCGCTTTGGGTAAATCTGACAATTGTACTTTGCATTATCATCTTCA	2880
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QY	2881	 TCCTTTCCGGTGATGGGAATGCAACTCTTCGGAAAAGAATTATCATGATCACAAGGACCGCT	2940	
Dd	2941	 TTCCGGATGGGACCTGCCGCGCTGGAACATTACACGACCTTTATGCACAGCTTCATGATCG	3000	
QY	2941	 TTCCGGATGGGACCTGCCGCGCTGGAACATTACACGACCTTTATGCACAGCTTCATGATCG	3000	
Dd	3001	 TGTTCCGGGTGCTCTCGGAGAATGATCGAGTCCATGTGGGACTCGATCFAGCTGGCGG	3060	
QY	3001	 TGTTCCGGGTGCTCTCGGAGAAATGATCGAGTCCATGTGGGACTCGATCFAGCTGGCGG	3060	
Dd	3061	 ATGCTCTCGTGCAATTCCTTCTCTTGGCCACCCTGTCATCGGCAATCTTGTGGTACTTA	3120	
QY	3061	 ATGCTCTCGTGCAATTCCTTCTCTTGGCCACCCTGTCATCGGCAATCTTGTGGTACTTA	3120	
Dd	3121	 ACGTTTTCTTAGCTTGTCTTTTGTGTCAAATTTTGGCTCATCTAGCTTATCAGCGCCGACTG	3180	
QY	3121	 ACGTTTTCTTAGCTTGTCTTTTGTGTCAAATTTTGGCTCATCTAGCTTATCAGCGCCGACTG	3180	
Dd	3181	 CGGATAACCATACGAATAAAATAGCCGAGGCCCTTCAATCGAATTGGCCGATTTTAAAGTT	3240	
QY	3181	 CGGATAACCATACGAATAAAATAGCCGAGGCCCTTCAATCGAATTGGCCGATTTTAAAGTT	3240	
Dd	3241	 GGGTTAAGCGTAAATATGTGCTGATTGTTTCAAAGTTAATACGTAAACAAATTCACAAAAATCAA	3300	
QY	3241	 GGGTTAAGCGTAAATATGTGCTGATTGTTTCAAAGTTAATACGTAAACAAATTCACAAAAATCAA	3300	
Dd	3301	 TAAGTGATCAACCATCAGGTGAGAGGACCAACAGATCAGTTGGATTTGGAGCGGAAGAGC	3360	
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QY	3541	 TGATTTGGCAACTCAATTACCCAGACAAATAGACTGGAACACGAGCTAAACCATAGAG	3600	
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Dd	3661	 GACCATTTCAAGGACGAGAGCCACAAGGGCAGCCGAGAGACGATGGAGGGCGAGGAGAACG	3720	
QY	3661	 GACCATTTCAAGGACGAGAGCCACAAGGGCAGCCGAGAGACGATGGAGGGCGAGGAGAACG	3720	
Dd	3721	 GGACGCCAGCAAGGAGGATTTAGGTCTCGACGAGGAACCTGGACGAGGGCGGAATCGG	3780	
QY	3721	 GGACGCCAGCAAGGAGGATTTAGGTCTCGACGAGGAACCTGGACGAGGGCGGAATCGG	3780	
Dd	3781	 AGGAGGGCCGCTCGACGCTGATATCATTTATTCACACACGACGAGGATATACTCGATG	3840	
QY	3781	 AGGAGGGCCGCTCGACGCTGATATCATTTATTCACACACGACGAGGATATACTCGATG	3840	
Dd	3841	 AATATCCAGCTGATTCGCTGCCCGGATTCGTACTATTAAGAAATTTCCGATCTTAGCCGGTG	3900	
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Db	6181	CGCCCGCTGCTGGAGATGTTAAACGGTACTCAGAACGAGTGCCTGATGCCGATG	6240
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RESULT	4	DROSODCHA	6883 bp mRNA INV 28-SEP-1993
LOCUS		Drosophila melanogaster para locus, sodium channel alpha subunit	
DEFINITION		mRNA, complete cds.	
ACCESSION		M32078 M24285 M32080	
NID		9403441	
KEYWORDS		alternative splicing; opa repetitive sequence; sodium channel alpha subunit.	
SOURCE		D.melanogaster (strain para-hd2), cDNA to mRNA, clone ZS10.3.	
ORGANISM		Drosophila melanogaster	
REFERENCE		Eukaryotae; Mitochondrial eukaryotes; Metazoa; Arthropoda; Tracheata; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.	
REFERENCE		1 (bases 1 to 6883)	
AUTHORS		Lounney,K., Kreber,R. and Ganetzky,B.	
TITLE		Molecular analysis of the para locus, a sodium channel gene in Drosophila	
JOURNAL		Cell 58, 1143-1154 (1989)	
MEDLINE		89376565	
REFERENCE		2 (sites)	
AUTHORS		Ramaswami,M. and Tanouye,M.A.	
TITLE		Two sodium channel genes in Drosophila: Implications for channel diversity	
JOURNAL		Proc. Natl. Acad. Sci. U.S.A. 86, 2079-2082 (1989)	
MEDLINE		89184571	
REFERENCE		3 (sites)	
AUTHORS		Thackeray,J.R. and Ganetzky,B.	
TITLE		Developmentally regulated alternative splicing generates a complex array of Drosophila para sodium channel isoforms	
JOURNAL		Unpublished (1993)	
COMMENT		Draft entry and computer-readable sequence for [Proc. Natl. Acad. Sci. U.S.A. 58, 1143-1154 (1989)] kindly submitted by B.Ganetzky, 25-APR-1989.	
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CDS

... Note: remainder of annotations omitted.

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QY 3667 TCAAGGACGAGAGCCACAAGGCGAGCGCCGAGAGCATGTGAGGGCGAGGAGAAGCGGACG 3726  
Db 3930 CCAGCAAGGAGGATTTAGGTCTCGACGAGGAACCTGGACGAGGAGGGCGAATGCGAGGAG 3989  
QY 3727 CCAGCAAGGAGGATTTAGGTCTCGACGAGGAACCTGGACGAGGAGGGCGAATGCGAGGAG 3786  
Db 3990 GCCCGCTCGAGGATATCATATTAATCATGCACACGAGGAGATATCTCGATGAATATC 4049  
QY 3787 GCCCGCTCGAGGATATCATATTAATCATGCACACGAGGAGATATCTCGATGAATATC 3846  
Db 4050 CAGGTGATTGCTGCCCGATTCTGTAATAGAAATTTCCGATCTTACCGCGGTGACGATG 4109  
QY 3847 CAGGTGATTGCTGCCCGATTCTGTAATAGAAATTTCCGATCTTACCGCGGTGACGATG 3906  
Db 4110 ACTGCCGCTTGGCAGGATGGGCAATTTACGACTGAAAACCTTTTCGATTAATTCAGG 4169  
QY 3907 ACTGCCGCTTGGCAGGATGGGCAATTTACGACTGAAAACCTTTTCGATTAATTCAGG 3966  
Db 4170 ATAATATTTTGAACACGCTGTTATCACTATGATTTTAAATGAGTAGCTTAGCTTTGGCAT 4229  
QY 3967 ATAATATTTTGAACACGCTGTTATCACTATGATTTTAAATGAGTAGCTTAGCTTTGGCAT 4026  
Db 4230 TAGAAGATGTACATCTGCCCAAGACCCATCTGCAGGATATTTTATCTATATGAGCA 4289  
QY 4027 TAGAAGATGTACATCTGCCCAAGACCCATCTGCAGGATATTTTATCTATATGAGCA 4086  
Db 4290 GAAATATTACGGTTATATCTCTTGGAAATGTTAATCAAGTGTGGCGCTCGGCTTCA 4349  
|||||

QY 4087 GAATATTTACGGTTATATTTCTTCTGGAATGTTAATCAAGTGGTTGGCGCTCGGCTTCA 4146  
Db 4350 AAGTGTACTTTGACCAAGCGGTGTGTGGCTGATTTCTGTTGTTGTCATGGTATCGCTTA 4409  
QY 4147 AAGTGTACTTTGACCAAGCGGTGTGTGGCTGATTTCTGTTGTTGTCATGGTATCGCTTA 4206  
Db 4410 TCAACTTTCTGTTGCTTCACTTTGTTGGAGCTGGTGTATTTCAAGCCCTTCAAGACTATCGGAA 4469  
QY 4207 TCAACTTTCTGTTGCTTCACTTTGTTGGAGCTGGTGTATTTCAAGCCCTTCAAGACTATCGGAA 4266  
Db 4470 CGTTAAGACACTGAGACCACTAGCTGCCATGTCCCGTATGCGAGGCGATGAGGGTGGTCG 4529  
QY 4267 CGTTAAGACACTGAGACCACTAGCTGCCATGTCCCGTATGCGAGGCGATGAGGGTGGTCG 4326  
Db 4530 TTAATGCGCTGGTACAAGCTATACCGTCCCATCTTCAATGTGCTATTGGTGTGCTAATAT 4589  
QY 4327 TTAATGCGCTGGTACAAGCTATACCGTCCCATCTTCAATGTGCTATTGGTGTGCTAATAT 4386  
Db 4590 TTTGGCTAAATTTTGGCCATAATGGGTGTACAGCTTTTGTGCGAAATATTTTAAAGTGGC 4649  
QY 4387 TTTGGCTAAATTTTGGCCATAATGGGTGTACAGCTTTTGTGCGAAATATTTTAAAGTGGC 4446  
Db 4650 AGGACATGAATGGCAGCAAGCTCAGCCACGAGATCATACCAATCGCAATGCCCTGCCGAGA 4709  
QY 4447 AGGACATGAATGGCAGCAAGCTCAGCCACGAGATCATACCAATCGCAATGCCCTGCCGAGA 4506  
Db 4710 GCGAGAACTACACGTGGTGAATTCAGCAATGAATTTTCGATCATGTAGTAAACGCGTATC 4769  
QY 4507 GCGAGAACTACACGTGGTGAATTCAGCAATGAATTTTCGATCATGTAGTAAACGCGTATC 4566  
Db 4770 TGTGCTTTTCCAAAGTGGCCACCTTCAAAGGCTGGATACAAATCATGAACGATGCTATCG 4829  
QY 4567 TGTGCTTTTCCAAAGTGGCCACCTTCAAAGGCTGGATACAAATCATGAACGATGCTATCG 4626  
Db 4830 ATTACGAGAGGTTGACCAAGCAACCAATTCGTGAAGCAACATCTACATGATTTATAT 4889  
QY 4627 ATTACGAGAGGTTGACCAAGCAACCAATTCGTGAAGCAACATCTACATGATTTATAT 4686  
Db 4890 TCGTATTTCTTCATATATTTTGATCATTTTTTTCACACTCAATCTGTTTTCATTTGGTGTATCA 4949  
QY 4687 TCGTATTTCTTCATATATTTTGATCATTTTTTTCACACTCAATCTGTTTTCATTTGGTGTATCA 4746  
Db 4950 TTGATAATTTTAAAGCAAAAGAAAGCAAGGAGGAGTGGATCATTAGAAATGTTTCATGACAG 5009  
QY 4747 TTGATAATTTTAAAGCAAAAGAAAGCAAGGAGGAGTGGATCATTAGAAATGTTTCATGACAG 4806  
Db 5010 AAGATCAGAAAAGTACTATAGTGTATGAAAAGATGGGCTCTAAAAAACCATTTAAAG 5069  
QY 4807 AAGATCAGAAAAGTACTATAGTGTATGAAAAGATGGGCTCTAAAAAACCATTTAAAG 4866  
Db 5070 COATTTCCAAAGCAAGGTTGGGACCAAGCAATAGTCTTTGAAATAGTAAACCGGATAAGA 5129  
QY 4867 CCATTTCCAAAGCAAGGTTGGGACCAAGCAATAGTCTTTGAAATAGTAAACCGGATAAGA 4926  
Db 5130 AATTGATATATCATTTATGTTATTTATTTTCATTTGCTGAACATGTTCCACCATGACCTTCGATC 5189  
QY 4927 AATTGATATATCATTTATGTTATTTATTTTCATTTGCTGAACATGTTCCACCATGACCTTCGATC 4986  
Db 5190 GTTACGATCGCTCGGACACGTATAACGGGGTCTAGACTATCTCAATCGGATTTTCGTAG 5249  
QY 4987 GTTACGATCGCTCGGACACGTATAACGGGGTCTAGACTATCTCAATCGGATTTTCGTAG 5046  
Db 5250 TTATTTTCAGTTCCGAATGCTATTAAAATATTCGCTTTAGGATATCAGTATTTTATG 5309  
QY 5047 TTATTTTCAGTTCCGAATGCTATTAAAATATTCGCTTTAGGATATCAGTATTTTATG 5106  
Db 5310 AGCCATGAATTTATTTGATGTAGTGTGTCATTTTATCCATCTTAGTCTGTGACTTA 5369  
QY 5107 AGCCATGAATTTATTTGATGTAGTGTGTCATTTTATCCATCTTAGGCTGTGACTTA 5166  
Db 5370 GCGATATTATCAGAAAGTACTTCGTGTCCGCCACCCCTGCTCCGAGTGGTGGGGA 5429  
QY 5167 GCGATATTATCAGAAAGTACTTCGTGTCCGCCACCCCTGCTCCGAGTGGTGGGGA 5226  
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Db	5430	AACTGGCGCGTGTCTTTCGACCTGGTGAAGGAGCCAAAGGGCAATTTCGGACACTGCTCTTCG	5489
Qy	5227	AACTGGCGCGTGTCTTTCGACCTGGTGAAGGAGCCAAAGGGCAATTTCGGACACTGCTCTTCG	5286
Db	5490	CGTTGGCCATGTGCGTTCGGCGGCCCTGTTCAACATCTGCTGCTGCTCTGTTCTCGTGCATGT	5549
Qy	5287	CGTTGGCCATGTGCGTTCGGCGGCCCTGTTCAACATCTGCTGCTGCTCTGTTCTCGTGCATGT	5346
Db	5550	TCATCTTTGCCATTTTCGGCATGTCTGTTCTTCATCGACGTGAAGGAGGAAGAGCGGCATTA	5609
Qy	5347	TCATCTTTGCCATTTTCGGCATGTCTGTTCTTCATCGACGTGAAGGAGGAAGAGCGGCATTA	5406
Db	5610	ACGACGCTTACAACITCAAGACCTTTGGCCAGAGCATGATCCTGCTTTTCAGATGTCGA	5669
Qy	5407	ACGACGCTTACAACITCAAGACCTTTGGCCAGAGCATGATCCTGCTTTTCAGATGTCGA	5466
Db	5670	CGTCAGCCGGTTGGATGGTGTACTGGACGCCATTATCAATGAGGAAGCATGGATGCCAC	5729
Qy	5467	CGTCAGCCGGTTGGATGGTGTACTGGACGCCATTATCAATGAGGAAGCATGGATGCCAC	5526
Db	5730	CCGACAAACGACAAAGGCTATCCGGGCAATGTGGTTCAGCGACCGTTGGAAATACGTTTC	5789
Qy	5527	CCGACAGCACAAAGGCTATCCGGGCAATGTGGTTCAGCGACCGTTGGAAATACGTTTC	5586
Db	5790	TCCTCTCATACCTAGTTATTAAGCTTTTTCATAGTTATTAAATATGATATGCTGTGCATTC	5849
Qy	5587	TCCTCTCATACCTAGTTATTAAGCTTTTTCATAGTTATTAAATATGATATGCTGTGCATTC	5646
Db	5850	TCGAGAACTATAGTCAGGCCACCGAGGACGTGCAAGAGGGTCTTAACCGACGACGACTACG	5909
Qy	5647	TCGAGAACTATAGTCAGGCCACCGAGGACGTGCAAGAGGGTCTTAACCGACGACGACTACG	5706
Db	5910	ACATGACTATGAGATCTGGCAGCAATTCGATCCGGAGGGGCAACCCAGTACATAGCTATG	5969
Qy	5707	ACATGACTATGAGATCTGGCAGCAATTCGATCCGGAGGGGCAACCCAGTACATAGCTATG	5766
Db	5970	ATCAGCTGTCCGAATTCCTGGAGCTACTGGAGCCCCGCTGCAGATCCCAAAACCCGAACA	6029
Qy	5767	ATCAGCTGTCCGAATTCCTGGAGCTACTGGAGCCCCGCTGCAGATCCCAAAACCCGAACA	5826
Db	6030	AGTACAAGATCATATCGATGGACATACCCATCTGTTCGGGTGACCTCATGTACTTGGCTCG	6089
Qy	5827	AGTACAAGATCATATCGATGGACATACCCATCTGTTCGGGTGACCTCATGTACTTGGCTCG	5886
Db	6090	ACATCCTCGACGCCCTTACGAAAGACTTCTTTTTCGGGGAAGGGCAATCCGATAGAGAGA	6149
Qy	5887	ACATCCTCGACGCCCTTACGAAAGACTTCTTTTTCGGGGAAGGGCAATCCGATAGAGAGA	5946
Db	6150	CGGCTGAGATTGTTGAGATAGCGGCCCGCCGGATACGAGGGGTACGAGCCGCTCTCAT	6209
Qy	5947	CGGCTGAGATTGTTGAGATAGCGGCCCGCCGGATACGAGGGGTACGAGCCGCTCTCAT	6006
Db	6210	CAACGCTGTGGGCTCAGCGTGAAGGATACTGCGGCCGGCTTAATCCAGACGCTTGGCGAA	6269
Qy	6007	CAACGCTGTGGGCTCAGCGTGAAGGATACTGCGGCCGGCTTAATCCAGACGCTTGGCGAA	6066
Db	6270	AGCACAAAGCGCGCGGAGGAGTGGTCTTTTGACCCGGATACGGATCATATGGCGATG	6329
Qy	6067	AGCACAAAGCGCGCGGAGGAGTGGTCTTTTGACCCGGATACGGATCATATGGCGATG	6126
Db	6330	GCGGTGATCCGGATGCGGGGACCGCGGCCCGGATGAAGCAACGAGCGGGATGCGGCCG	6389
Qy	6127	GCGGTGATCCGGATGCGGGGACCGCGGCCCGGATGAAGCAACGAGCGGGATGCGGCCG	6186
Db	6390	CTGGTGGAGATGTTAGTGTAAACGTTACTGCAAGAGGAGCTGCCGATGCCGATGAGAGTA	6449
Qy	6187	CTGGTGGAGATGTTAGTGTAAACGTTACTGCAAGAGGAGCTGCCGATGCCGATGAGAGTA	6246
Db	6450	ATGTAATAGTCCGGGTGAGGATGCAGCGCGCGCGGACAGCAGCAGCAGCAGCGCGCG	6509
Qy	6247	ATGTAATAGTCCGGGTGAGGATGCAGCGCGCGCGGACAGCAGCAGCAGCAGCAGCGCG	6306

Db	6510	CGGGGGCAGCAGCAGCGCGGGAAGTCCCGAGCGGGTAGCGCCGGCGGACAGACCGCCG	6569
Qy	6307	CGGGGGCAGCAGCAGCGCGGGAAGTCCCGAGCGGGTAGCGCCGGCGGACAGACCGCCG	6366
Db	6570	TTCTCGTGGAGCGACGGGTTCTGTGACGAAGACGCCACAAAGTGGTATCCACATCGC	6629
Qy	6367	TTCTCGTGGAGCGACGGGTTCTGTGACGAAGACGCCACAAAGTGGTATCCACATCGC	6426
Db	6630	GATCGCCGAGCATCACGTCCGCGCAGCGGGATGCTGTGAGCCAGCGCTCGCCCCCTCC	6689
Qy	6427	GATCGCCGAGCATCACGTCCGCGCAGCGGGATGCTGTGAGCCAGCGCTCGCCCCCTCC	6486
Db	6690	AAGATGCACGCGATTATAGC	6710
Qy	6487	AAGATGCACGCGATTATAGC	6507
RESULT	5		
LOCUS	MDU38813	6318 bp	19-FEB-1997
LOCUS	Musca domestica insecticide-susceptible strain	INW	
DEFINITION	sodium channel mRNA, complete cds.		
ACCESSION	U38813		
NID	g1783372		
KEYWORDS	house fly.		
SOURCE	Musca domestica		
ORGANISM	Eukaryotae; mitochondrion; eukaryotes; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha; Muscoidea; Muscidae; Musca.		
REFERENCE	1 (bases 1 to 6318)		
AUTHORS	Knipple,D.C., Doyle,K.E., Marsella-Herrick,P.A. and Soderlund,D.M.		
TITLE	Tight genetic linkage between the kdr insecticide resistance trait and a voltage-sensitive sodium channel gene in the house fly		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 91 (7), 2483-2487 (1994)		
MEDLINE	94195766		
REFERENCE	2 (bases 1 to 6318)		
AUTHORS	Ingles,P.J., Adams,P.M., Knipple,D.C. and Soderlund,D.M.		
TITLE	Characterization of voltage-sensitive sodium channel gene coding sequences from insecticide-susceptible and knockdown-resistant house fly strains		
JOURNAL	Insect Biochem. Mol. Biol. 26 (4), 319-326 (1996)		
MEDLINE	96245434		
REFERENCE	3 (bases 1 to 6318)		
AUTHORS	Ingles,P.J., Adams,P.M., Knipple,D.C. and Soderlund,D.M.		
TITLE	Direct Submission		
JOURNAL	Submitted (17-OCT-1995) Dave M. Soderlund, Entomology, New York State Agricultural Experiment Station, Cornell University, Castle Street, Geneva, NY 14456, USA		
REFERENCE	4 (bases 1 to 6318)		
AUTHORS	Ingles,P.J., Adams,P.M., Knipple,D.C. and Soderlund,D.M.		
TITLE	Direct Submission		
JOURNAL	Submitted (15-JAN-1997) Dave M. Soderlund, Entomology, New York State Agricultural Experiment Station, Cornell University, Castle Street, Geneva, NY 14456, USA		
REMARK	Nucleotide and protein update by submitter		
FEATURES	Location/Qualifiers		
source	1. 6318		
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	/strain="NAIDM"		
	/note="insecticide-susceptible reference strain"		
	/db_xref="taxon:7370"		
	/chromosome="3"		
	1. 6318		
	/codon_start=1		
	/product="voltage-sensitive sodium channel"		
	/db_xref="PID:g1783373"		
CDS	/translation="MTEDSDSISEERSLRFPTRESLQIEQIAIEHEKQERLKR		
	AAGEQIRYDEDEGQPDQLEQVPIVRMQGSPPELASTPLEDIDPFYSNVL		
	TFYVSKQDIDFRFSASKAMWLDPNPIRRVAIYILVHPLSLFIITLTILNCILM		
	MPPTTVESTVEIFTGTITFESAVKVMKGFILCPFTYLRDANWLDVFIAYLWTH		
	GIDLGNLAALRTRVLRALKTAIVLPGKTIVGAVIESVKNRDLVILTFVSUVAL		
	MGLQIYMVDYKICRIFRPLDGGWNLNTDENWFLHNSNSNFTWDFWEDLSYPCVGNV		
	GAGCGGEGVTCLOGICRPNPDYDTSDFSGFASRLMTQDFWEDLYHQVLAQAAG		



QY	1827	GATGCCAGACACTTGGCCCTATGCCGACGACTCGAATGCCTCACCCCGATGTCCGAA	1886
Db	1828	GAGAATTGGTGCCATTATAGTACCAGCCTACTATTGTAAATTAGTTTCTAGACATTCTTCA	1887
QY	1887	GAGATTGGGCCATCATATGTCCTGGTGTAATGGCAATCTAGCTCCGACACTCATCG	1946
Db	1888	TATACCTCGCATCAATCAAGAACTCTGTAATACATACATGATGTGAATTATTGGGTGGCATG	1947
QY	1947	TATACCTCGCATCAGTCCCGAAATATCGTATACCTCACATGCGCATCTACTCGGCGCATG	2006
Db	1948	CGGSCCATGGTGCCAGACAATGACCAAGAGAGCAAAATGCCAGCTGCCACACACGC	2007
QY	2007	GCGGTATGGGCTGAGCAACAATGACCAAGGAGACAAATTCGCGAACCCGCAACACACGC	2066
Db	2008	AATCAATCAATCGGTGCTCGAACCAATGGTGCGCATAGTAGCGGTGGTGGGTATPCCC	2067
QY	2067	AATCAATCAGT--GG-GC-CCCAACCAATGGCGCACCA--C-CTG-TC-TGGNCA--CC	2114
Db	2068	GATGCCAATCACAAAGAACAAAGGATTATGAATGGGTGAGGATTATACAGACGAGACT	2127
QY	2115	AATCAACAAGTCT---GATCATCGGACTACGAAATGGCCCTGGAGTGCACGGACGAGCT	2171
Db	2128	GGCAAAATAAACACACACACAATCCTTTATTCGAGCCCCGTCCAACACTCAAACAGTGGTA	2187
QY	2172	GGCAAGATTAAACATCATGACAATCCTTTATTCGAGCCCCGTCCAAGACAAAACGGTGGT	2231
Db	2188	GACATGAAGATGTTATGTGCTTTAAATGATATCATTTGAACAAGCCGTGGTGGSCATAGT	2247
QY	2232	GATATGAAGATGTTGATGTCTGTAATGACATCATCGAACAGGCCGTGGTGGCACAGT	2291
Db	2248	CGTCTAGTGAACGAGGTG-----AGGACGATGACGAAGAT	2283
QY	2292	CGGCAAGCGATCGCGGTGTCTCCGTTTTACTATTTCCTCAACAGAGGACGATGACGAGAT	2351
Db	2284	GGTCCACATTCGAAGACATCGCCCTCGAATACATCTTAAAGGCATCGAAATCTTTGT	2343
QY	2352	GGGCGGAGTTCAAGACAAAGGCATCGAAGTGATGCTCAAGGCATCGATGTGTTGT	2411
Db	2344	GTATGGACGTGTTGTGGGTGGTTTAAATTTCAAGAAATGGGTGTCCTTTATTGTGCTC	2403
QY	2412	GTGTGGACGTGTTGCTGGGTGGTTGAAATTTCAAGAGTGGGTATCGCTCATCGCTTC	2471
Db	2404	GATCCATTCTGGAGCTCTTCATTACCCCTGTGTTATGGTCAATACGATGTTTATGGCC	2463
QY	2472	GATCCCTTCGTCGAGCTCTTCATCAGCTGTGCATTGTGGTCAACAGATGTTCTATGGCA	2531
Db	2464	ATGATCATCACACATGAATCCGGNAITTAGAAGAGTGTGTGAAGAGTGAATTTTC	2523
QY	2532	ATGATCACCACGATATGAACAAAGGAGATGGAAACGCGTCTCAAGAGTGGCAACTATTC	2591
Db	2524	TTACAGGCCACTTTTGCATTGAAGCCACATGAACATGATGGCCATGAGCCGCAAGTAC	2583
QY	2592	TTACGCCCACTTTGCGATFCGAGGCCACCATGAAGCTAATGGGCATGAGCCCCAAGTAC	2651
Db	2584	TACTTCCAGGAAGCTGGAACTTTTCGATTTCATTATTGTGGCCCTGCTCTCTGCTGAA	2643
QY	2652	TATTTCCAGGAGGCTGGAACATCTTCGACTTCATTATCTGGCCCTATCGCTATTGGAA	2711
Db	2644	TTGGCCCTGGAGGTGTCCAGGCCCTGTCGGTGTGTGAGAAGTTTTCGTTGCTTCGTGTA	2703
QY	2712	CTGGGACTCGAGGTGTCCAGGCTCTGTCGGTATTGCGGTTCCTTTTCGATTGCTCGGTGA	2771
Db	2704	TTCAAAATGGCAAAATCATGGCCCCACACTCAATTTACTCATTTTCGATTATGGGCGGACA	2763
QY	2772	TTCAAACTGGCCAAAGTCTTGGCCCCACACTTAATTTACTCATTTTCGATTATGGGACGACC	2831
Db	2764	ATGGGTGCATGGGTAACTGCACATTTGTACTTTGCAATTTGCAATATCATCTTCATCTTTCGCGTG	2823
QY	2832	ATGGGCGCTTTGGGTAACTGACATTTGTACTTTGCAATATCACTTCATCTTTTCGCGTG	2891
Db	2824	ATGGGAATGCAACTTTTCGGAAAGAACTATATTGACCACAAAGGATTCGCTTCAAGGACCAT	2883

Qy	2892	ATGGGAATGCACTGTTCCGGAAGAATAATATCATGATACAAAGGACCGCTTTTCCGGATGGC	2951
Db	2884	GAATTACCGCGCTGGAACTTCACCGACTTTCATGSCACAGCTTCATGATGTGTTCCCGAGTG	2943
Qy	2952	GACCTGCGCGCTGGAATTCACCGACTTATATGCACAGCTTCATGATGCTTCCGGGTG	3011
Db	2944	CTGTGCGGAGATGGATCGAGTCCATGTGGGACTGCATGTATGTGGGGCGATGTCACTGT	3003
Qy	3012	CTCTGCGGGAATGGATCGAGTCCATGTGGGACTGCATGTACGTGGGCGATGTCTCGTGC	3071
Db	3004	ATACCCCTTCCTTGTGGCCAGCGTGTATAGCAATCTTGTGGTTCTTAATCTTTTCTTA	3063
Qy	3072	ATTCCTCTCTCTTGGCCACCGTGTCACTGGCAATCTTGTGTACTTTAACTTTTCTTA	3131
Db	3064	GCCTTGTCTTTGTCCAACTTCGGTCTCATCTAGTCTTATCAGCCCCGACTGCGCGACAATGAT	3123
Qy	3132	GCCTTGTCTTTGTCCAAATTTTGGCTCATCTAGCTTATCAGCGCGACTGCCGATAACGAT	3191
Db	3124	ACCAATTAATATAGCAGAGGCTTCAATCTGATTGTCTGTTTTAAGAACTGGGGTGAACGT	3183
Qy	3192	ACGAATTAATATAGCGAGGCTTCAATCGAATTTGGCCGATTTAAAAGTTGGGTTAAAGCGT	3251
Db	3184	ATAATTCCCGATTGTTTTAAGTTAATTCGAATAAATTCAGACAATCAATAAGTGACCAA	3243
Qy	3252	AATATTGCTGATTGTTTCAAGTTAATACGTACAAATTTGACAAATTCAAATTAAGTGATCAA	3311
Db	3244	CCATCAG-----A-A-CA-----TGG--CGAT-A--ATG-----	3265
Qy	3312	CCATCAGGTGAGGACCACAGATCAGTTGGATTGGGCGAAGACGATGGTGACAA	3371
Db	3266	-AACTGGAGTTGGGTCAATGACGAAATCATGGCGATGCTTGATCAAAAAGGGTATGAAG	3324
Qy	3372	GAACTGGAGCTGGGCCACGACGAGATCTCTCGCGAGGCCCTCATCAAGAAGGGGATCAAG	3431
Db	3325	GCGCAGACCCAGCTGGAGGTGGCCATTCGGGATGCGATGGAGTTCCACCATACATGCGCAT	3384
Qy	3432	GAGCAGACGCAACTGGAGGTGGCCATTCGGGGATTCGGATGGAATTCACCATACACGGCGAC	3491
Db	3385	ATGAAAACCAACAGCGAAGAATCAAAATTCATGAACAACAACAACGATGATTGGAAC	3444
Qy	3492	ATGAAGAACACACGCGAGAATCCAAATATCTAATTAACGCAACCGATGATTGGCAAC	3551
Db	3445	TCATAAACCAACCAAGACAAATAGACTGGAAACATGAGCTAAACCATAGAGGTTGTGCCATA	3504
Qy	3552	TCAATTAACCAACCAAGACAAATAGACTGGAAACACGAGCTAAACCATAGAGGTTGTGCCATA	3611
Db	3505	CAGACGATGACACTGCCACATTAACCTCATATGTTAGCCATAAAGATTCGACCATCAAG	3564
Qy	3612	CAGACGACGACACTGCCACATTAACCTCATATGTTAGCCATAAAGATTCGACCATCAAG	3671
Db	3565	GACGAGACCAAGGCGACGCGAGACCATCTGAGGGGAGAGAAACGGCAGCTCAGC	3624
Qy	3672	GACGAGACCAAGGCGACGCGAGACCATCTGAGGGGAGAGAAACGGCAGCTCAGC	3731
Db	3625	AAAGAGGACCTTCGSCCTCGACGAGGAACCTGGACGAGGAGCGCGAGGGGATGAGGGCCAG	3684
Qy	3732	AAGGAGGATTAGTCTCTGACGAGGAACCTGGACGAGGAGGCGGAATGCGAGGAGGCGCG	3791
Db	3685	CTGATGGTGACATTATCATTCATGGCGAAAACGACGACGAGATTAATCGACGACTATCCG	3744
Qy	3792	CTCAGCGGTGATATCATTAATTCATGACA---CGACGAGGATATATCTCGATGAATATCCA	3848
Db	3745	GCCGACTGTTTCCCGACTCGTACTACAAGAGTTTCCGATCTTGGCCGGGACACGAGAC	3804
Qy	3849	GCTGATTGCTGCCCGGATTGCTACTATAGAATAATTTCCGATCTTAGCCGGTGACGATGAC	3908
Db	3805	TCGCGCGTCTCGCAAGGATGGGCAATTTACGACTGAAAACCTTTTCAATTAATTTGAAAAT	3864
Qy	3909	TCGCGCGTCTCGCAAGGATGGGCAATTTACGACTGAAAACCTTTTCAATTAATTTGAAAAT	3968
Db	3865	AAATATTTGAAACCGCAGTTATCACTATGATTTTAATGAGTAGCTTAGCTTGGCCCTTA	3924
Qy	3969	AAATATTTGAAACAGCTGTATCACTATGATTTAATGAGTAGCTTAGCTTGGCAATTA	4028



Db	3925	GAAGATGTTTCATTTACCGGATGACCTGTCATGCAGGATATACTCTACTACATCGACAGG	3984
Qy	4029	GAAGATGATATCTGCACAAAGACCCTACTGCGAGGATATTTATATCTATATGGACAGA	4088
Db	3985	ATATTTACGGTGATATCTTTTTGGAGATGTTGTATCAAAATGGTTGGCCCTGGGCTTTAAG	4044
Qy	4089	ATATTTACGGTTATATCTTCTTGGAAATGTTAATCAAGTGGTTGGCGCTCGCTCAA	4148
Db	4045	GTTTTACTTCACCAATGCGCTGGGTGGCTGGATTTCTGATTCATGCTATACGCTTATA	4104
Qy	4149	GTGTACTTTCACCAACGCGGTGGTTGGCTCGAATTTTCGTGATTCATGATTCGCTTATC	4208
Db	4105	AAITTTGGTTCCGCTTTGGTCGGGCTTTAAATGATATAGACCGTGTTTAGATCAATCGCACA	4164
Qy	4209	AACTTCGTTGCTTCACTTGTGGAGCTGGTGTATTCAGGCTTCAAGACTATCGGAACG	4268
Db	4165	CTGGCGCCCTAAGGCCATTTGGCTGCTCTAGATGGGAGGATATGAAAGTTTGTCTGT	4224
Qy	4269	TTAAGACACTAGACACCACTACGTGCATCTCCCTGATTCAGAGGCATGAGGGTCTGCTT	4328
Db	4225	AATCGCTGCTTCAAGCTATACCGTCATCTTCAATGTCATTTGGTGGTGTGCTGATATTT	4284
Qy	4329	AATCGCTGCTACAGCTATACCGTCCATCTTCAATGTCATTTGGTGGTGTGCTGATATTT	4388
Db	4285	TGGCTATTTTTGCCATTTATGGAGTACAGCTTTTTTGGCTGGAAATATTTTAAAGTATAA	4344
Qy	4389	TGGCTAATTTTTGCCATAATGGGTGTACAGCTTTTTTGGCTGGAAATATTTTAAAGTGGAG	4448
Db	4345	GATGGTAATGACACTGTCTGAGCCATGAAATCATACCGAATCGTATGCTCGCAAAAGT	4404
Qy	4449	GACATGAATGGCAGCAAGCTCAGCCACGAGATCATACCAATCCGAATGCTCGCAGAGC	4508
Db	4405	GAAACTTACACTCGGGAATTTCCGCAATGAACTTCGATCATGTAGTATGCGTATCTC	4464
Qy	4509	GAGAACTACAGTGGGTGAATTCAGCAATGAATTCGATCAATGATGAGTACGCGTATCTG	4568
Db	4465	TGCTATTTCAAGTGGCCACCTTTAAGGCTGGATCCAGATTTATGAACGATGCCATTTGAT	4524
Qy	4569	TGCTTTTCCAACTGGCCACCTTCAAGGCTGGATACAAATCATGAACGATGCTATCGAT	4628
Db	4525	TCAGGAGGTGGACAAGCAGCGCATCCGAGAAACCAATATCTACATGTATTTATATTTTC	4584
Qy	4629	TCAGGAGGTGGACAAGCAACCAATTCGTGAACGACACATCTACATGTATTTATATTTTC	4688
Db	4585	GTATTTCTCATATATTTGGATCATTTTTCACACPCAATCTGTTTCATTTGGTGTATCATTT	4644
Qy	4689	GTATTTCTCATATATTTGGATCCTTTTTCACACTCAATCTGTTTCATTTGGTGTATCATTT	4748
Db	4645	GATAATTTTAAAGCAAAAGAAAGAAAGCTGGTGATCATTTAGAAATGTTTCATCGACAGAA	4704
Qy	4749	GATAATTTTAAAGCAAAAGAAAGAAAGCAAGTGATCATTTAGAAATGTTTCATCGACAGAA	4808
Db	4705	GATCAGAAAAGTACTATAATGCTATGAAAAGATGGGCTCTAAAAACCAATATAAAGCC	4764
Qy	4809	GATCAGAAAAGTACTATAATGCTATGAAAAGATGGGCTCTAAAAACCAATATAAAGCC	4868
Db	4765	ATTCCAGACCGAGGTGGCGACCAACGAATAGTATTCGAAATAGTTCAGATATAAAAA	4824
Qy	4869	ATTCCAGACCAAGTGGCGACCAACGAATAGTCTTTGAAATAGTAAACCGATAAGAAA	4928
Db	4825	TTCGATATATCATATGTTGTTTCATTTGGCTTTAAACATGTTTACCATGACCCCTGATCGG	4884
Qy	4929	TTCGATATATCATATGTTTATTCATTTGGCTGACATGTTTACCATGACCCCTGATCGT	4988
Db	4885	TACGACGCTCGAGCGGTACAAACGAATGCTCTGACAAACTCAATGGGATATTCGTAGTT	4944
Qy	4989	TACGATCGCTCGACACGATTAACCGGCTCTAGACTATCTCAATGCGATATTCGTAGTT	5048
Db	4945	ATTTTCAGTGGCGAATGCTATTTAAATAATTTCCGTTTACGATATCACTATTTTCAAGAG	5004
Qy	5049	ATTTTCAGTTCCGAATGCTATTTAAATAATTTCCGTTTACGATATCACTATTTTATTTGAG	5108

Db	5005	CCATCGGAATTTATTGTAAGTAGTAGTGTCAATTTATCACTTATAGGCTTGTACTACGAC	5064
QY	5109	CCATCGGAATTTATTGTAAGTAGTAGTGTCAATTTATCCATCTTATAGGCTTGTACTTACG	5168
Db	5065	GACATCATTTGAGAAGTATTTCCGTATCCGCGACACACTGCTCCGCTGCGTGAGAGTGCCGAAA	5124
QY	5169	GATATTATCGAGAAGTACTTCTGTGTCCGCGACCTCTCCGAGTGGTGGTGCGGAAA	5228
Db	5125	GTGGGTGCGTGTCCCTGCTTTAGTCAAGGGTGGCAAGGGTATCCGGACAGCTTGTCTGTCCGCG	5184
QY	5229	GTGGCGCGTGTCCCTGCTACACTGGTGAAGGGAGCCAAAGGGCATTCGCGACACTGCTCTTCGCG	5288
Db	5185	TTAGCCATGTGGTGTCCGCTGCTTTATTCACATTTTGTCTGTCTGCTGCTTTGGTGATGTTCT	5244
QY	5289	TGGCCATGTGCGTGTCCGCGCCCTGTTTCAACATCTGCGCTGCTGCTTCTCTGGTCAATGTTCT	5348
Db	5245	ATCTTTGCTATCTTTTGGCATGTCCCTTCTTCATCGCATGTCAAAGAGAAGAGCGGCATAAAT	5304
QY	5349	ATCTTTGCCATTTTCGGCATGTCTGTTCTTCATGCGAGTGAAGGAGCAAGCGCGCATTAAC	5408
Db	5305	GCTGTGTATAATTTTAGACACATTTGGCCAAAGTAGTAGATATGCTGCTGTTTCAGATGCTACCC	5364
QY	5409	GACGCTCTACAACCTTCAAGACCTTTGGCCAGAGCATGATCTGCTCTTCAGATGCTCGACG	5468
Db	5365	TCAGCCGGTGGGATGGTGTGTAGATGCCATTTATCAATGAGGAAGATTGCGATCCACCC	5424
QY	5469	TCAGCGGTTGGGATGGTGTACTGACGAGCCATTTCAATGAGGAAGCAATGCGATCCACCC	5528
Db	5425	GACAAACGACAAAGGCTATCCGGGCAATTTGTGGTTTCAGCGACTGTTTGGAAATACGTTTCTC	5484
QY	5529	GACACGACAAAGGCTATCCGGGCAATTTGTGGTTTCAGCGACCGCTTGGAAATAACGTTTCTC	5588
Db	5485	CTTTCATATCTAGTATAAGCTTTTGTAGTAGTATTATATGTACATTTGCTGTCAATCTCTC	5544
QY	5589	CTCTCATACCTAGTATTAAAGCTTTTGTAGTAGTATTATATGTACATTTGCTGTCAATCTCTC	5648
Db	5545	GAGAACTATAGCCAGGCTACGGAGGATGTACAGGAGGGTCTCACCGACGACGATTACGAT	5604
QY	5649	GAGAACTATAGTCAGGCCACCGAGGACGTGCAAGAGGTTCTAACCGACGACGACTAGAC	5708
Db	5605	ATGTACTACGAGATTTGGCAACAATTCGATCCGGAGGGACCCAGTACATACGCTAGCAC	5664
QY	5709	ATGTACTATGAGATCTGGCAGCAATTCGATCCGGAGGGACCCAGTACATACGCTATGAT	5768
Db	5665	CAGCTGTCCGAGTTTCTGGACGTCGTGGAGCCGCGCTGCAGATCCACAAGCCGAACAAG	5724
QY	5769	CAGCTGTCCGAATTCCTGGACGTTACTGGAGCCGCCCTGCAGATCCACAACCCGAACAAG	5828
Db	5725	TACAAATCATATCGATGACATGCCGATATGTCCGGGGACATGATGATCTGTGTGGAT	5784
QY	5829	TACAAGATCATATCGATGGACATACCCATCTCTCGCGGTGACCTCATGTACTGCGGTGCAC	5888
Db	5785	ATATTGGATGCCCTGACCAAGGACTTCTTTGGCGCAAGGGTAAATCCGATCCGAGGACG	5844
QY	5889	ATCTTCAGCCGCTTACGAAAGACTTCTTTGGCGGAAGGCAATCCGATAGAGGAGACG	5948
Db	5845	GGTGAATTTGGTAGATAGCGCGGACCGACACCGAGGCTATGATCCGGGTGCTGCA	5904
QY	5949	GGTGAGATTGGTAGATAGCGCGCCCGCCGGATACGGAGGGCTACGAGCCCGTCTCATCA	6008
Db	5905	ACACTGTGGCGCAGCGTGGAGGACTCTCGGCCAAGCTGATACAGAAATCGGTGGCG	5960
QY	6009	ACGCTGTGGCGTCAGCGTGAGGAGTACTGCGCCCGGCTAAATCCAGCAGCGCTGGCG	6064
RESULT	6		
LOCUS	MDPARA	6899 bp	RNA
DEFINITION	M.domestica mRNA for voltage-sensitive sodium channel, complete	INV	17-SEP-1996
ACCESSION	CDS		
NID	X96668		
KEYWORDS	voltage-sensitive sodium channel.		
SOURCE	house fly.		



ORGANISM	Musca domestica	Best Local Similarity 84.9%; Pred. No. 0.00e+00;
	Eukaryota; Mitochondrial eukaryotes; Metazoa; Arthropoda;	Matches 4986; Conservative 0; Mismatches 806; Indels 84; Gaps 22;
	Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera;	
	Muscomorpha; Muscoidea; Muscidae; Musca.	
REFERENCE	1 (bases 1 to 6899)	
AUTHORS	Williamson,M.S., Martinez-Torres,D., Hick,C.A. and Devonshire,A.L.	
TITLE	Identification of mutations in the housefly para-type sodium channel gene associated with knockdown resistance (kdr) to pyrethroid insecticides	
JOURNAL	Mol. Gen. Genet. 252 (1-2), 51-60 (1996)	
MEDLINE	96397509	
REFERENCE	2 (bases 1 to 6899)	
AUTHORS	Williamson,M.S.	
TITLE	Direct Submission	
JOURNAL	Submitted (15-MAR-1996) M.S. Williamson, IACR-Rothamsted, Department of Biological & Ecological Chemistry, Harpenden, Hertfordshire, AL5 2JQ, UK	
FEATURES	Location/Qualifiers	
source	1..6899	
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BASE COUNT	1965 a 1445 c 1660 g 1829 t	
ORIGIN		
Query Match	56.4%; Score 3676; DB 14; Length 6899;	

QY 1227 GGACCATGGCACATCGTGTCTTTATAGTCAATCATCATCTTCTCAGTTCATTCTATCTTGTG 1286  
Db 1244 AATTGTATTTGGCCATTGTTGCCATCTTATGACGAATTGCAAAAGAAAGCGCGAAGAA 1303  
QY 1287 AATTGTATTTGGCCATTGTTGCCATCTGCTATGACGAATTGCAAAAGAAAGCGCGAAGAA 1346  
Db 1304 GAAGAGCTCGCGAGGAGGCGGATACGAGAGAGCTGAAGAGGCGAGCAGCGCAAGGCG 1363  
QY 1347 GAAGAGCTCGCGAGGAGGCGGATACGTAAGCGGAAGAGTGCCTCGCGCGCAAGCG 1406  
Db 1364 GCCAACTGGAGAGCGGCGCAATGTAGCAGCTCAAGCGCTCAGGATCGACGGGATGCC 1423  
QY 1407 GCCAAGCTGGAGAGCGGCGCAATGCCAGGCTCAGGACGAGCGGATGCGGTGCGCGC 1466  
Db 1424 GCTCGGCGAGCTGCGATCCCGAGATGGCAAGAGTCCCAAGTCTTTCATTTAGCTAT 1483  
QY 1467 GAAGAGCTGCATCGCATCCGGAATGGCCAGAGTCCGAGCTATCTTGCATCAGCTAT 1526  
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QY 1527 GAGCTATTTGTGGCGGCGAGAGGCGCAAGATGACAAACAAAGAGAGATGTCCATT 1586  
Db 1544 CGCAGCTGCAAGTGAATCGGAGTCCGTGAGCGTTATACAAAGACACACGACCTACC 1603  
QY 1587 CGGAGCGTGCAGGTGGAGTCGGAGTCGGTGAGCGTTATACAAAGACAAACGACCTACC 1646  
Db 1604 ACAGCAC-CC--GCTACTAAAGTCCGTAAAGTTAGCAGGACTTCTTATCCTTACCTGGT 1660  
QY 1647 ACAGCACCAAGCTACCAAGTTCGTAAGTGAGCAGCAGACATCTTATCCTTACCTGGT 1706  
Db 1661 TCACCATTTAACCTACCGCGGGATACAGTAGTTTCACACAAGTACACAATACGAATGGG 1720  
QY 1707 TCACCGTTTAAACATACGAGGGGATACAGTAGTTCTCACAAAGTACAGGATACGGAAGCG 1766  
Db 1721 CGTGACGTTTGTGTATACAGGTAGCGATCGCAAGCCATTGCTGCTGCAACATATCAG 1780  
QY 1767 CGTGCGCGCTTGTGTATACCGGTAGCGATCGTAGCCATTGGTATTGTCAACATATCAG 1826  
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QY 1827 GATCCCCAGCAGCATTTGCCCTATGCCGAGCAGCTCGAATGCCGTACCCCGCATGTCCGAA 1886  
Db 1841 GAGAAATGGTGCCATTATGATACAGCCTACTATTGTAAATTTAGTTCTAGACATTTTCA 1900  
QY 1887 GAGAAATGGGCCATCATAGTGCCTGTACTATGSCAATCTAGGCTCCCGACACATCATCG 1946  
Db 1901 TATACCTCGCATCAATCAAGAATCTCGTATACATCAGATGGTGAATTTATGGGTGGCATG 1960  
QY 1947 TATACCTCGCATCAGTCCCGAATATCGTATACCTCAGATGCCGATCTACTCGGCGGCATG 2006  
Db 1961 GCGGCCATGGTGCCAGCACAAATGACCAAGAGAGCAAAATTTGCCAGTTCGCAACACACGC 2020  
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Db 2021 AATCAATCAATCGGTGTGCNACCAATGTGGGAGTAGTACGGCCGGTGGTGGGTATFCCA 2080  
QY 2067 AATCAATCAGT-GG-GC-GCCACCAATGGGCGCCACCAC--CTGTC--TGGA--C-A-CCA 2115  
Db 2081 GATGCCAATCACAAGGAACAAAGGATTTGAAATGGTGGTGGTGGTGGTGGTGGTGGTGGT 2140  
QY 2116 -ATCACAGCTC---GATCATCGCATACGAAATTTGGCTGGAGTGCAGCGGAGGAGCT 2171  
Db 2141 GGCAAAATAAACACACGACAATCTCTTTATCGAGCCCGTCCAAACTCAAAAGTGGTA 2200  
QY 2172 GGCAAGATTAACATCATGACAATCTCTTTATCGAGCCCGTCCAGACACAAACGCGTGT 2231  
Db 2201 GACATGAAGATGTATGGCTTAAATGATATCATTTGAACAAGCCGCTGGTGGCATAGT 2260  
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Db 2297 GGTCCACACATTCAGGACATCGCCCTCGAATATATCCTTAAAGGATCGAAATCTTTGT 2356  
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QY 2472 GATCCCTTCTCGAGCTCTTCATCAGCTGTGCAITTTGGTCAACACGATGTTTCATGGCA 2531  
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QY 2532 ATGGATCACCAGATATGAACAGGAGATGGRAAGGTCCTCAAGAGTGGCAACATTTTC 2591  
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QY 3072 ATTCCTTCTTCTTGCCACCGTTGTCATCGGCAATCTTTGTGTAATTAACCTTTCTTA 3131  
Db 3077 GCTTGTCTTTGTCCAACTTCGGTTCATCTAGTTTATAGCCCCGACTGCCGACATGAT 3136  
QY 3132 GCTTGTCTTTGTCCAAATTTTGGCTCATCTAGCTTTATCAGCGCCGACTGCCGATACGAT 3191  
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QY 3312 CCATCAGGTGAGAGGACCAACCAAGTTCAGTTGGAGCGAAGAGATGGTGAAC 3371  
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Qy	5589	CTCTCATACCTAGTTATAAGCTTTTGTGATAGTTTATTAATATGATACATTGCTGCTCATCTC	5648
Db	5558	GAGAACTATACCCAGGCTACGAGGATGTACAGAGGGTCTCACCGAGCAGGATTAGCAT	5617
Qy	5649	GAGAACTATAGTACAGGCCACCGAGGAGCTGCAAGAGGGTCTTAACCGAGCAGCATTAGCAT	5708
Db	5618	ATGTACTACGAGATTTGGCAACAATTCGATCCGAGGGCACCCAGTAGTACATAGAATACGAC	5677
Qy	5709	ATGTACTATGAGTCTGCACCAATTCGATCCGAGGGCACCCAGTAGTACATACGCTATGAT	5768
Db	5678	CAGCTGTCCGAGTTTCTGGACGTGCTGGAGCGCCGCTGACAGTCCACAGCCGAAACAAG	5737
Qy	5769	CAGCTGTCCGAAATCTTGGACGTACTGGAGCGCCGCTGACAGTCCACAAACCGAAACAAG	5828
Db	5738	TACAAATCATATCGATCGACATCCGATATGTCGGGGCGACATGATCTACTGTGTGGAT	5797
Qy	5829	TACAAGATCATATCGATCGACATCCCATCTGTCCGGTGACCTCATGTACTGCTGCTGAC	5888
Db	5798	ATATTGGATGCCCTGACCAAGGACTTCTTTGCGGCGCAAGGGTAATCCGATCGAGGAGCG	5857
Qy	5889	ATCCTCGAGCCCTTACGAAAGACTTCTTTGCGGCGCAAGGGCAATCCGATAGAGGAGCG	5948
Db	5858	GGTGAATTTGGTGAATTTGGCGCGCGCGCGACACCGAGGCGCTATGATCCGGTGTCTGCG	5917
Qy	5949	GGTGAATTTGGTGAATTTGGCGCGCGCGCGCGATACGAGGCGCTATGATCCGGTGTCTGCA	6008
Db	5918	ACACTGTGCG	5973
Qy	6009	ACCGTGTGCG	6064
RESULT	7		
LOCUS	MDU38814	6315 bp mRNA	INV 19-FEB-1997
DEFINITION	Musca domestica insecticide-resistant strain voltage-sensitive sodium channel mRNA, complete cds.		
ACCESSION	U38814		
NTD	g1842213		
KEYWORDS	house fly.		
SOURCE	Musca domestica		
ORGANISM	Eukaryotes; mitochondrial eukaryotes; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha; Muscoidea; Muscidae; Musca.		
REFERENCE	1 (bases 1 to 6315)		
AUTHORS	Knipple,D.C., Doyle,K.E., Marsella-Herrick,P.A. and Soderlund,D.M.		
TITLE	Tight genetic linkage between the kdr insecticide resistance trait and a voltage-sensitive sodium channel gene in the house fly		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 91 (7), 2483-2487 (1994)		
MEDLINE	94195766		
REFERENCE	2 (bases 1 to 6315)		
AUTHORS	Ingles,P.J., Adams,P.M., Knipple,D.C. and Soderlund,D.M.		
TITLE	Characterization of voltage-sensitive sodium channel gene coding sequences from insecticide-susceptible and knockdown-resistant house fly strains		
JOURNAL	Insect Biochem. Mol. Biol. 26 (4), 319-326 (1996)		
MEDLINE	96245434		
REFERENCE	3 (bases 1 to 6315)		
AUTHORS	Ingles,P.J., Adams,P.M., Knipple,D.C. and Soderlund,D.M.		
TITLE	Direct Submission		
JOURNAL	Submitted (17-OCT-1995) Dave M. Soderlund, Entomology, New York State Agricultural Experiment Station, Cornell University, Castle Street, Geneva, NY 14456, USA		
REFERENCE	4 (bases 1 to 6315)		
AUTHORS	Ingles,P.J., Adams,P.M., Knipple,D.C. and Soderlund,D.M.		
TITLE	Direct Submission		
JOURNAL	Submitted (15-JAN-1997) Dave M. Soderlund, Entomology, New York State Agricultural Experiment Station, Cornell University, Castle Street, Geneva, NY 14456, USA		
REMARK	Nucleotide and protein update by submitter		
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DILYIMDRIFTVIFLEMLIKALGFKVYFTNACWDLDFVIMLSLNLVAVHSGLN			
DIAYFRSMRTLRLALPLRAVSRWEGKVVVNAVQAFISFNVLVLIILFVILFIM			
VOLFAGKYFKCKDNDTVLSHEIIPNRACKSENITWENSANFEDHGNVLCFQVA			
TFKGTQIMDAIDREVDKQIRETNIYMYLFFVFFIFGSEFTLNFIVLIDNFN			
EOKKAGSGLEMETDOKKYVNAKMGSKKPLAIPRPWRPQAIIVEIVTDKDF			
IIMLPIGLNEMFTLDYDASEAVNNVLDKNGLFVVFSECECLKIFALRYHYKE			
PWNLFDDVVVLSLGLVLSLIEKIFVSPILLRVVRVAKVGRVLRVLRKAGKIGTLL			
FALMSLPALFNLCILLLFVMEIFAIGMSFFHMKESGINAVNFKTFGSGMILLF			
QMSAGMDGVLDIAIINEEDCPDPNDKXGPGCSATVIGTIFLLSYLVISLVINM			
YIATILENSQATSEVDQGLTDDYDIMEIQWDFPEGTQYIRYDQSEFJDLVLEPP			
LOIHPNKYKIIISMDPICRGDMYICVDILDALTQDFARKGNPEIETGEIQAAR			
DTGYDVPVSTLWROREYCAKLIQNAWRKYKNGPOEGDEGAAGGDEGAGGEG			
GSGGGDDGGSATAGATPTDPAAGEADGASAGNGGGLSPGCVSGSGNQRTAVL			
VESDGVTKNGHVKVHSRSPITSITADV"			
BASE COUNT	1711 a	1344 c	1595 g 1665 t
ORIGIN			
Query Match	56.3%	Score 3664;	DB 14; Length 6315;
Best Local Similarity	84.8%	Pred. No. 0.00e+00;	
Matches	4980;	Conservative 0;	Mismatches 812; Indels 84; Gaps 21;
Db	151	ATACGATATGATGACGAGGACGAGATGAAGGTCACAGCCGATCCACACTTGAACAG	210
QY	207	ATCCGATATGATGACGAGGACGAGGATGAAGTCCACACCGGATCTACACTTGAACAG	266
Db	211	GGTGTGCTTACCTGTTTCGAATGCAGGGCAGCTTCCGGCGGAATGGCTCCACTCCT	270
QY	267	GGTGTGCCAATACCTGTTTCGATTCGAGGCGAGCTTCCGGCGGAATGGCTCCACTCCT	326
Db	271	CTCGAGGATATCGATCCCTCTTACAGTAATGTACTGACATTTGTAGTAATAAGTAAAGGA	330
QY	327	CTCGAGGATATCGATCCCTCTTACAGCAATGTACTGACATTCGTAGTTGTAAACCAAGGA	386
Db	331	AAGGATATTTTTCGTTTCTTCGCTCAAAAGCAATGTGGTGTCTGCATTCATTCAATCCG	390
QY	387	AAAGATATTTTTCGCTTTCTTCGATCAAAAGCAATGTGGATGCTGCATTCATTCAATCCG	446
Db	391	ATACGTCGTAGCCATTATATTTTACTGCATCCCTTGTTCGTTTATTCATTATCAACC	450
QY	447	ATACGTCGTGTGCCATTATACATTCATGCATCCATTTTTCCTTATTCATCATCAACC	506
Db	451	ACTATTCTTAACTAATTTGATTTTAAATGATATGCGCAACGCCACGGTCGATCCACA	510

QY 507 ACAATTCTCGTCAACTGCATCCCTGATGATTAATGCCGACACGCCACGGTTGAGTCCACT 566  
Db 511 GAGGTGATATTCACCGGAATCTACACATTTGAATCAGCTGTTAAAGTGTGAGCAGGAGT 570  
QY 567 GAGGTGATATTCACCGGAATCTACACATTTGAATCAGCTGTTAAAGTGTGAGCAGGAGT 636  
Db 571 TTCAATTTATGCCCGTTAGCTATCTTAGAGATGCAATGGAATTTGGCTGGACTTCGTAGTA 630  
QY 627 TTCAATTTATGCCCGTTAGCTATCTTAGAGATGCAATGGAATTTGGCTGGACTTCGTAGTA 686  
Db 631 ATAGCTTTAGCTTATGTGACCATGGGCATAGATTTAGTAAATCTCGCAGCTTTGAGAACA 690  
QY 687 ATAGCTTTAGCTTATGTGACCATGGGTATAGATTTAGTAAATCTAGCAGCCCTGCGNACG 746  
Db 691 TTTAGGTAAGTGTGAGCTCTGAAACCGTAGCCATTTGTGCCAGGTCTAAACCAATTTGTC 750  
QY 747 TTTAGGTAAGTGTGAGCTCTGAAACCGTAGCCATTTGTGCCAGGTCTGAAAGACCATCGTC 806  
Db 751 GGTGCTGTCAATTAATCTGTAATAAATCTAGCGATGTGATAATTTTGACAATGTTTTC 810  
QY 807 GGGCCGCTCATGAATCGGTGAAGATCTCGCGATGTGATTAATCTGACCATGTTTCTCC 866  
Db 811 CTGTGCGTGTTCGGCTGATGGGCTACAAATCTATATGGTGTCTTAACACAAAAGTGC 870  
QY 867 CTGTGCGTGTTCGGCTGATGGGCTACAAATCTATATGGTGTCTTAACACAAAAGTGC 926  
Db 871 ATTAAGCATTTCCCTCGAGCGAGTTGGGCAATCTGACCATGAATACTGGTTCTTA 930  
QY 927 ATCAAGAAGTTCCCGCTGGAGCTTCTCGGGCAATCTGACCGACGAGAACTGGGACTAT 986  
Db 931 CACAATAGCAACAGTTCCCAATTTGGTTTACGGAGAACAGTGGCGAGTCAATTCGGTGTGC 990  
QY 987 CACAATGCGCAATAGTCCCAATTTGGTTTACGGAGAACAGTGGCGAGTCAATTTCCGTTATGC 1046  
Db 991 GGAATGATATCCGTGCGGACCAATGGCGGAAGATTAACCTCTGCCTGCGAGGCTTCGCG 1050  
QY 1047 GGAATATATCCGTGCGGGAATGGCGAGCATTAACCTCTGCCTGCGAGGCTTCGTTGGT 1106  
Db 1051 CCAATCCCAACTACGACTACACAGTTTCGACTCAATTCGGTTGGGCTTTCCGTGTGGCG 1110  
QY 1107 CCGAATCCGAATATGGCTACACAGCTTCGATTCGATCGTTCCGATGGGCTTTCTGTCCGCC 1166  
Db 1111 TTTGCTCATAGCAACCAAGATTTCTGGGAGGATCTGATCAGCAGCTGCTGCAAGCAGCT 1170  
QY 1167 TTCGGCTGATGACAGAGGACTTCTGGGAGGATCTGATACAGCTGCTGTTGCGCGCGCC 1226  
Db 1171 GGACCTGGCACATGTTGTTCTTATAGTCAATCATCTTCCTAGTTCATTTCTATCTTGTG 1230  
QY 1227 GGACCATGGCACATGCTGTTCTTATAGTCAATCATCTTCCTAGTTCATTTCTATCTTGTG 1286  
Db 1231 AATTGATTTTGGCCATGTTGGCATGCTTATGACCAATTCGAAAGAGAGGCGCGAAGAA 1290  
QY 1287 AATTGATTTTGGCCATGTTGGCATGCTGATGACCAATTCGAAAGAGAGGCGCGAAGAA 1346  
Db 1291 GAGAGGCTGCGGAGGAGGAGGCGATCCGAGAGCTGAAGAGCGGAGCGGACGCGCAAGCG 1350  
QY 1347 GAGAGGCTGCGGAGGAGGAGGCGATACGTGAAGCGGAAGAGCTGCGCGCGCGCAAGCG 1406  
Db 1351 GCCAACTGGAGGAGGCGGCAATGTAGCAGCTCAAGCGCTCAGGATGACGGGATGCC 1410  
QY 1407 GCCAAGCTGGAGGAGGCGGCAATGCCAGGCTCAGGACGCGGATGCGGCTGCGCGCC 1466  
Db 1411 GCTCGGCGAGCTCTGCATCCGAGATGGCAAGAGTCCCGAGTCTCTTCATTAGCTAT 1470  
QY 1467 GAAGAGCTGCATCTGCATCCGGAATGGCCAGAGTCCGAGCTATTTTGCATCAGCTAT 1526  
Db 1471 GAATGTTTGTGGCGGAGAGGCGACGATGACAAACAAAGAGAGAGATGTCGATA 1530  
QY 1527 GAGCTATTTGTGGCGGAGAGGCGACGATGACAAACAAAGAGAGATGTCATT 1586  
Db 1531 CGAGCGTCAAGTGGAAATCGGAGTCGGTATGAGCTTTATACAAGACCAACGACCTACC 1590  
QY 1587 CGGAGCGTCAAGTGGAGTCGGAGTCGGTATGAGCTTTATACAAGACCAACGACCTACC 1646

Db 1591 ACAGCAC-CC--GCTACTAAAGTCCGTAAGTTAGCAGCACTTCCTTATCTTACCTTGGT 1647  
QY 1647 ACAGCACACCAAGCTACCAAAAGTTCGTAAGTGCAGCAGACATCTTATCTTACCTTGGT 1706  
Db 1648 TCACCAATTTAACTAGCTAGCCGGGATCAGCTAGTTTACACAAAGTACACAATACGAATGGG 1707  
QY 1707 TCACCGTTTAAACATCGCAGGGGATCAGCTAGTTTCTCAAAAGTACAGTACGGAACGGA 1766  
Db 1708 CGTGGACGTTTTGGTATACAGGTAGCTAGCAGCCATTCGTAAGTTCGTAACATATCAG 1767  
QY 1767 CGTGGCGGCTTTGGTATACCCGGTAGCGATCTGAAGCCATTTGGTATTTCAACATATCAG 1826  
Db 1768 GATGCCACAGAGATTTGGCCCTATGCCGATGACTCGAATTCGCGTAAACCAATATGTCGAA 1827  
QY 1827 GATGCCACAGAGCACTTGCCCTATGCCGAGCACTCGAATTCGCGTACCCCGATGTCGAA 1886  
Db 1828 GAGAATGGTGCCATTAATAGTACCAGCCTACTATTGTAATTTAGGTTCTAGACATTTCTCA 1887  
QY 1887 GAGAATGGGGCCATCATAGTGGCCGTGTACTATGGCAATCTAGGCTCCGACACTCATCG 1946  
Db 1888 TATACCTCGCATCAATCAAGAATCTCGTATACATCACATGGTGTGATTTATGGTGGCATG 1947  
QY 1947 TATACCTCGCATCAGTCCCGAATATCGTATACCTACATGGCGATCTACTCGCGCGATG 2006  
Db 1948 GGGCCCATGGGTGCCAGCAATGACCAAGAGAGCAAAATTCGCGAGTCCGCAACACACGC 2007  
QY 2007 GCGCTCATGGCGTCAAGCAATGACCAAGAGAGCAAAATTCGCGAACCAGCAACACACGC 2066  
Db 2008 AATCAATCAATCGGTGCTGCAACCAATGGTGGCAGTAGTACGGCCGGTGGTGGCTATGCC 2067  
QY 2067 AATCAATCAAT--GG-GC-GCCACCAATGGCGCACAC--CTGTC--TGGA--C-A--CC 2114  
Db 2068 GATGCCAAATCACAAGAACAAAGGATTTAATGAATGCGTCAGGATTTATACAGACGAAGCT 2127  
QY 2115 AATCACAGTCT---GATCATCGGACTACGAAATTTGGCTTGGAGTGCAGGACGAAGCT 2171  
Db 2128 GGCATAATAAACACCAACCAACATCTTTATCGAGCCGCTCCAAACTCAAAACAGTGGTA 2187  
QY 2172 GGCAGATTAACATCATGACAACTCTTTATCGAGCCGCTCCAGACACAAACGGTGGT 2231  
Db 2188 GACATGAAGATGTTATGCTTTAAATGATATCATTTGAACAGCCGCTGGTGGCGATG 2247  
QY 2232 GATATGAAGATGATGATGCTGTAATGATCATCATGAACAGCCGCTGGTGGCGACAGT 2291  
Db 2248 CGTCTAGTGAACGAGTG------AGCAGCATGACGAGAT 2283  
QY 2292 CGGCAAGCATCGCGGTGTCCTCGTTTACTATTTCCCAACAGAGGACGATGACGAGAT 2351  
Db 2284 GGTCCACATTTCAAGGACATCGCCCTCGAATATATCTTAAAGGCAATCGAAATCTTTTGT 2343  
QY 2352 GGGCCGACGTTCAACACAGGCACTCGAAGTATCTCTCAAGGCACTGATGTTTGT 2411  
Db 2344 GTATGGACTGTTTGGTGGTGGTTAAATTTCAAGATGGGTCTCTTTTATTTGTTTC 2403  
QY 2412 GTTGGGACTGTTGCTGGGTTTGGTTGAAATTTTCAGGAGTGGTATCGCTCATCTCTTC 2471  
Db 2404 GATCCATCTGTGAGCTCTTCAATCCCTGCTGTTGTTGTTCAATACATGTTTCATGGCC 2463  
QY 2472 GATCCCTTGTGAGCTCTTCAATCGCTGTCATTTGTTGTTCAACAGATGTTTCATGGCA 2531  
Db 2464 ATGGATCATCACACATGAATCCGGAATTTGGAGAAGTGTCTGAAAGTGGTAACTATTTTC 2523  
QY 2532 ATGGATCACCACCATATGAACAGGAGATGGAACGGTGTCTCAAGAGTGGCACTATTTTC 2591  
Db 2524 TTCAGGCCACTTTTCAATTTAGGCCAGCATGAATACTGATGCCATAGCCCCGCAAGTAC 2583  
QY 2592 TTCACGCCACCTTTGCCATCGAGGCAACCATGAAGCTAATGGCCATAGSCCCCAAGTAC 2651  
Db 2584 TACTTCCAGGAAGCTTGAACATTTTCGATTTTCAATTTATGTTGGCTTGTCTCTGCTGGAA 2643  
QY 2652 TATTTCCAGGAGGCTGGAACATCTTCGACTTCAATTTATGTTGGCCCTATGCTATTGGAA 2711









YCARLIONAWRKHQROGAPGEDSDEAGDDPELQDRHTAVLVESDGFVTKNGHRVV

IHSRSPSVTSRSTVD\*

BASE COUNT 1615 a 1376 c 1531 g 1574 t

ORIGIN

Query Match 29.4%; Score 1912; DB 14; Length 6096;

Best Local Similarity 71.2%; Pred. No. 0.00e+00;

Matches 4180; Conservative 0; Mismatches 1578; Indels 115; Gaps 74;

Db	151	CGGTACGATGACGAGACCAAGATGAAGCCCTCAGCGGATGCGACTCTGAGCAAGG	210
Qy	210	CGATATGATGACGAGACGAGGATGAAGTCCACACCGGATCCTACATTTGAACAGG	269
Db	211	GCSCCATCCCTTCGCAATGCAAGCCCTTCCCTCCGAGCTCGCTCTACCCCGCTC	270
Qy	270	GTSCCAATACCTTGTGATGTCAGGCGAGCTCCCGCGGGAATGGCTCTCCACTCTC	329
Db	271	GAGGACATGACCCCTCTACCAACACGAGACAGATTTTGGTGGTGAGCAAGGAAG	330
Qy	330	GAGGATATCGATCCCTACTACAGCAATGTACTGACATTCGTATGTTGAAGCAAGGA	389
Db	331	GATATTTTCCGGTTCAGTCGAGAGATGCCATGTGATTTTGGACCCATTCAACCGG	390
Qy	390	GATATTTTCCGTTTCTGCAATCAAGCAATGTGATGCTCGATCCATCAATCGATA	449
Db	391	CGACGGGTGCCATCTACATTTTGGTTCACCCCTTGTCTCACTCTTCAATATACCAC	450
Qy	450	CGTGTGTGCCATTTACATTTCTAGTGCATCCATTTATTTCCCTATTCATCATCAC	509
Db	451	ATTTTAACCAACTGCATCTTCATGATCGCTTACACCCCAACCAATAGATCCACTG	510
Qy	510	ATTCTGTCAACTGCATCTTCATGATTAATGCCGACCAACGCCACGTTGAGTCC	569
Db	511	GTAATTTTACTGGCATCTACATTTGAATCGCGCTTAAAGTGATGCGAGAGGTTTC	570
Qy	570	GTGATTTACCGGAATCTACATTTGAATCAGCTTTAAAGTGATGCGACGAGTTTC	629
Db	571	ATACTTCAGCCATACAGTACCTTAGAGATGCATGGAATGGCTGGACTTCGTAGTA	630
Qy	630	ATTTTATGCCGTTTACGATCTTAGAGATGCATGGAATTTGGCTGGACTTCGTAG	689
Db	631	GCITTAGCTTACGTAATGCGGATAGATCTAGGAACCTGCGCCCTTGGCAAGCTTC	690
Qy	690	GCITTAGCTTATGACCATGGGTATAGATTTAGGTAATCTAGACCCCTCGGACGTT	749
Db	691	AGGTGCTCGGAGCTTTGAAGACTGTCGCTATTGTTCCAGGTTTGAAGACCATTTG	750
Qy	750	AGGTGCTCGGAGGCTTTAAACCGTAGCCATTGTGCCAGGCTTGAAGACCATCGT	809
Db	751	GCTGTGATGTAATCTGTAAGAACCTCGCGGATGTAATATCTCACCAGTTTCTGCT	810
Qy	810	GCCGTATCGAATCGGTGAAGAAATCTCGCGATGTGATTTATCTGACCATGTTCT	869
Db	811	TCCGTGTTTGGCTTAATGGGCTCCAGATTTACATGGGTGTCTCAGCGAAGTGCAT	870
Qy	870	TCGTGTTTGGCTTATGGGCTCACATCTATATGGGCGTGTCTCACCAGAGTGCAT	929
Db	871	AAAACTTCCCATTAATGTTTATGGGGGAATTTGAATGATGAGAACTGGCATGCA	930
Qy	930	AAGAATTTCCGCTGGAGGTTCTTGGGCAATCTGACCGACAGAACTGGGACTAT	989
Db	931	TGCAGTAAACACAGAACTGGTACTTTCCGGAAGTTCACCAAGAGTTCCACTGTG	990
Qy	990	AATCGCAATAGCTCCAATGGTATTTCCGAGGACGAGGGCATCTCATTTCCGTT	1049
Db	991	AATTCATCAGGAGCTGGTACATGTCACCTGATTACACATGTCTCCAGGGCTTGG	1050
Qy	1050	ATATATCCGGTGGGGCAATGCGACAGCAATACGTGTGCTCGACAGGTTTGGTC	1109
Db	1051	AATCCCACTATGTTACACAGTTTTCGATACGTTTGGTGGGCAATTCCTCTCGC	1110
Qy	1110	AATCCGAATTTATGCTACACAGCTTCGATTCGTTCCGATGGGCTTTCTCTCG	1169

Db	1111	AGACTGATGACCCAGGATTTATGGGAGAACCTTTATCAGCTGGTTTTGAGATCTGCTGG	1170
Qy	1170	CGGTGATGACACAGCACTTTCTGGGAGATCTGTACCAGCTGGTGTGGCGCGCGGA	1229
Db	1171	CCCTGGCATATGCTGTTCTTCAATTTGTCATCATCTCTTAGGCTCATCTATCTGTGA	1230
Qy	1230	CCATGGCAGATGCTGTTCTTATAGTCATCATCTCTTAGGCTCATCTATCTGTGA	1289
Db	1231	TTGATTTTGGCCATTTGTCGCAATGCTCTAGCATGAGTTGCAGAAAGCTGAGGAG	1290
Qy	1290	TTGATTTTGGCCATTTGTCGCAATGCTCTAGCATGAGTTGCAGAAAGCTGAGGAG	1349
Db	1291	GAACACCGGAAGAAAGCTTTAGGGAAGCGGAAGACAGCTCTTGCAGAAAGGCG	1350
Qy	1350	GAGCTGCCGAAGAGGAGGATACGTTGAAGCGGAAGAGCTGCCGCGCAAGCGGCC	1409
Db	1351	AAAAATTAAGACAAGCGGATAAACTGCG--AG--CACAAGAATTAGCAGCAGCACAG	1407
Qy	1410	AAGCTGGAGNGCGGCCAATGCCAGGCTCAGGCAGCGGATCGGCTGCCCGGAA	1469
Db	1408	CTAGCTGGCGCAATCTAGCAAAATCTCCCTCGG--GAAGT--TCGTCCTGT--AG	1464
Qy	1470	GAGCTGCACTGCATCCGGAATGGCCAAGAGTCCGACGATTTCTTGCATCAGCTATG	1529
Db	1465	TTGTTTATAAATCAAAAGGCGCAACAATCACAACAAAGGAGACATGAGCATCCG	1524
Qy	1530	CTATTTTGGCGGAGAGGCGAAGATGACAAACAAGAGAAAGTGTCCATTCGG	1589
Db	1525	AGCGA--AGGCGG---GGACTCGATAAGCGA--ACACAAAGG--AAG--AGTGG	1575
Qy	1590	AGCTGAGGTTGGAGTCGGAGTCGTCGAGGTTATACAAAGACAAACGACCTTACC	1649
Db	1576	GGT--ACG--GCGATCA--G---G--AAGTGAGCGCGGAAGTTTGGTCTACAGG	1626
Qy	1650	GCACACCAAGCTACCAAGTTCTGTAAGTGAGCAGCATCTTATCTTACCTGGTTC	1709
Db	1627	CCTTTCACCATCCCGAGTTCACCAAGGTAGTCATCATTACAAATTAGAACCGGAC	1686
Qy	1710	CCGTTTAAACATACGCGGGGATCAGTAGTTCTCACAAGTACACGATACGGAACG	1769
Db	1687	GGAAGTTTCGTGGGCCCCACCTGGTGGTATCGAAACCCCTTAGTACTTCTACGTC	1746
Qy	1770	GGCGCTT--TGGTAT--ACCGGTAGCGATCGTAAGCCATTGGTATGTCAACATAT	1826
Db	1747	GATGACAAGAATCTTCTTATGTCAGATCAGTCAATGAGTAAACACCTATGTCAG	1806
Qy	1827	GATGCCAGCAGCACTTCCCTTATGCCGACACTCGAATCGCTCACCCCGATGTCCG	1886
Db	1807	GAGATGGAGCAATAGTTGTACCAAGTTTATACGCCAGCTCGGTTCCAGGCACTC	1866
Qy	1887	GAGATGGGCGCATCATAGTGGCGGTACTATGGCAATCTAGGCTCCCGACACTAT	1946
Db	1867	TATACATCACAGCATCCAGGATFCTTACAGTCTCATGGGACCTCCTGGGTG--CA	1924
Qy	1947	TATACCTCGCATCCTCCGAATATCGTATACCTCAGTGGGATCTACTCGGCGCAT	2006
Db	1925	GCAA--CAAA--C--TCAGACCA--GATCAATCA--A--C---TSCGAGCTCGT	1974
Qy	2007	GCGGTATGGGCGTCAGCAATGACCAAGGAGAGCAATTTGCCGAACCGCAACACG	2066
Db	1975	AA--CAACCTT-----CAC--A--GGTG--C--CTAA--T--TCT--ACACCAT	2018
Qy	2067	ATCAATCAGTGGGCGCCACCAATGGCGCACCACTGTCTGGACACCAATCACAAG	2126
Db	2019	G--TCAGCA--GAC--A--GTAT--GA--TGGAG-----CGGT--GAAA--AG	2059
Qy	2127	GATCTCGGCACTAGCAAAATTTGGCTGGAGTGCAGCAGAGAGTGGCAAGATT	2186
Db	2060	C--TGCAATCCATTCATGAACAAATGACGAAACTACAAATTTGTTGATATGATG	2118
Qy	2187	CATGACATCTCTTTATCGAGCCCTCCAGACACAAAGGTTGGTGTGATGATGAA	2246
Db	2119	ATGGTCTGAATGACATTTATAGAACAAAGCTGCTGGACAGCAGAGTAGAGCCAG	2178



Db	4304	CTTTGAGCCACGAAATCAATCTCTGACAGAAATGCTTGGCATTTGCTGAAAACTTACACATGGG	4363
Qy	4465	AGCTCAGCCACGAGATCATACCAAAATCGCAATGCGCTGGCAGGAGGAGAACTTACACGTGGG	4524
Db	4364	AGAACTCGCCAATGAATTTTGATCAGCTCGGCAGAAAGCTTATCTCTGCTCTTCCAAGTGG	4423
Qy	4525	TGAATTCAGCAATGAATTTTCGATCATGTAGTAAACGCGTATCTGTGCGCTTTTCCAAGTGG	4584
Db	4424	CCACCTTCAAAGGATGGATTCAGATCATGAATGAGCGCTATAGACTCTAGAGAGCTCCATA	4483
Qy	4585	CCACCTTCAAAGCTGGATACAAATCATGAACGATGCTATCGATTCAGAGAGGTGGACA	4644
Db	4484	AGCAGCCAATCAGGGAACGACATCTCATGTACCTCTACTTTGTGTCTTTTATCATCT	4543
Qy	4645	AGCAACCAATTCGTGAAGAGCAACATCTACATGTATTTATTTATTTCTCTTCATCATAT	4704
Db	4544	TTGGCTCATTTTTTCACTCTCAACCTATTCAATTTGGTGTGATCATCGACACAACTTTAATGAGC	4603
Qy	4705	TTGGATCCTTTTTTCACACCTCAATCTGTTTCATTTGGTGTATTCATTTGATTAATTTTAAAGC	4764
Db	4604	AAAAAGAAAAGCAGGAGGTGCTAGACATGTTTCATGACTGAAGATCAGAGAAATTAAT	4663
Qy	4765	AAAAAGAAAAGCAGGTGGATCATTAAGAAATGTTTCATGACAGAGATCAGAAAAAGTACT	4824
Db	4664	ACAAATGCTATGAAGAAATGGGTTGCAAAAAACCGTTAAAAAGCCATCCCCAGGCGCAAAAGT	4723
Qy	4825	ATAATGCTATGAAGAAAGATGGGCTCTFAAAAAACCATTTAAAGGCCATTCCTCAAGACCAAGT	4884
Db	4724	GGAGACCGCAGGCCATGTGTTTGAATCTGCACAGACAGAAATTTGACATGATCATCA	4783
Qy	4885	GGCAGCACAAAGCAATAGTCTTTTGAATATAGTAACCGATTAAGAAAATTCGATATAATCATTA	4944
Db	4784	TGTTGTTTCATTGGCTTTAAACATGTTAAACATGACACTCTGGATCACTATCAACAGCTGAAGC	4843
Qy	4945	TGTTATTCAATGGTCTGAACATGTTCCACATGACCTCGATCGTTACGATCGCTCGGACA	5004
Db	4844	AGTTACGCGACGTTCTTTGATTACTTGAACATGATCTTCATCGTCACTCTTCAGTTCGCGAGT	4903
Qy	5005	CGTATAACGCGGCTTAGACTATCTCAATGCGATATTCGTAGTTATTTTCAGTTTCGCGAAT	5064
Db	4904	GTCGTATGAAGATATTTCGCGCTCAGATACCACTACTTCAAGGAAACCATGGAACTCTTTG	4963
Qy	5065	GTCTATTAAAAAATTCGCTTTTACGATATCACTATTTATTATTGAGCCATGGAAATTTATTTG	5124
Db	4964	ATTTGCTAGTTGTCATCTATCTATTTGGGTCTGGTATTGAGTGAACATCAATTCAGAAAT	5023
Qy	5125	ATGTAGTAGTTGTCATTTTATCCATCTTAGTCTTTGTAAGCGATATTATCGAGAAGT	5184
Db	5024	ACTTTGTGTCGCCCTACACTGCTTCGAGTGGTGAGAGTGGCGAAGGTGGGTGCGATCCCTGC	5083
Qy	5185	ACTTCGTGTCCGCGACCTGCTCCGAGTGGTGGCTGTGGCGAAGGTGGCGCTGCTCTTC	5244
Db	5084	GTCGTGTGAAGGTGCTAGAGGTATTTCGACATATGCTGTTCGCTTGGCTATGCTTTTTC	5143
Qy	5245	GACTGTGTGAAGGAGGCGCAAGGGCATTCGACACACTGCTCTTGGCGTTGGCCATGTGCGTGC	5304
Db	5144	CAGCGCTCTTCAATATCTGCCCTACTACTATTTTATAGTCATGTTATTTTTCGCACTCTCG	5203
Qy	5305	CGGCGCTGTTCACACATCTGCGCTGCTGCTCTTCTGGTCACTGTTTCATCTTTGCCATTTTCG	5364
Db	5204	GCATGCTCTTCTTCATCGACGTCGCGGATTAAGGTGGCTTGTATGACGTGTACAAATTTCA	5263
Qy	5365	GCATGTGCTTCTTCATCGAGTGAAGGAGAGAGCGGCATTAACGACGCTTACAACTTCA	5424
Db	5264	AGACGTTTGGCAGTCCATGATCCTGCTCTTCCAGATGTCCACATCACTGAGTGGGATG	5323
Qy	5425	AGACCTTTGGCCAGAGCATGATCCTGCTCTTTTTCAGATGTGACAGCTCAGCCGCTGGGATG	5484
Db	5324	GTGTGTTTAGATGGGATCATGAATGAGAGGACTGCAACAAACCAATAGCCAGATTCGCT	5383
Qy	5485	GTGTACTGGAGGCCATTTCAATGAGGAAGCATGGATCCACCCGACAGCAACAAAGCT	5544

D	b	5384	ACCCGGGAGACHGTGGATCAGCACTACTGTGCGCATAGCTTTCTTGTGTCATACCTCGTCA	5443							
Q	y	5545	ATCCGGGCAATTGTGGTTCAGGACCGGTGGAATAACGTTTTCTCTCATACCTAGTAGTA	5604							
D	b	5444	TCAGTTTCTCTATTCTTATTAAACATGTACATGCFTGCTCATTTTGAGAAATTAATCTCCCAGG	5503							
Q	y	5605	TAAAGCTTTTGTATGATGTTATTATATGTACATTTGCTGTCAATCTCTCAGAACATATAGTCAGG	5664							
D	b	5504	CGACAGAGGATGTGCGAAGAAGCTTTGACGGGATGATGACTACGATATGTACTATGAAAATTT	5563							
Q	y	5665	CCACCGAGGACGTGCAAGAGGGTCTTAACCGAGGACGACTACGACATGTACTATGAGATCT	5724							
D	b	5564	GACAGAGTTTGACCACGATGGGACGCAATATATTTCGTATGACAGCTGTGGGATTTCC	5623							
Q	y	5725	GGCAGCAATTCGATCCGGAGGGCACCCAGTACATACGCTATGATCAGCTGCCGAATTC	5784							
D	b	5624	TCGACGTGCTGGAACCTCCGCTGCAGATACATAACCCGACAAGTACAAGATAGTGTGCA	5683							
Q	y	5785	TGGACGTACTTGGAGCCCCGCTGTCAGATCCCAAACCGACAAGTACAAGATCATATCGA	5844							
D	b	5684	TGGACATCTCCGATTCGCAAGGGGACCTCATGTTCTGTGTGGACATTTTGGATGCTTTGA	5743							
Q	y	5845	TGGACATACCCATCTGTGCGGTGACCTCATGTACTGCGTGACATCTCTGACGCCCTTA	5904							
D	b	5744	CGAAGGACTTCTTTTCAAGGAAGCAATCTTATAGAAGTCTTCGACAGTTGGGTGAAG	5803							
Q	y	5905	CGAAAGACTTCTTTTCGCGGAAGGCAATCCGATAGAGAGACGGTGAGATTGCTGAGA	5964							
D	b	5804	TCCAACCAAGGGGGCGGACGAAAGTGGCGTATGAGCCCTGTCTCTACGCTGTGGCGGC	5863							
Q	y	5965	T---AGCGGCGCGCGGATACGGAGGGCTACGAGCGGCTCTCATCAACGCTGTGCGGCTC	6021							
D	b	5864	ACCGAGAGAATAATTGTGCGGCACGTATACAGAAATGCATGGCGCAAGCACAAAG	5916							
Q	y	6022	ACCGTGAGGAGTACTGCGCCCGGCTTAATCCAGACGCTTGGGAAAGCACAAAG	6074							
<hr/>											
RESULT	9										
LOCUS	BGU73583	6096 bp	mRNA	INV 19-MAR-1997							
DEFINITION	Blattella germanica para sodium channel mRNA, complete cds.										
ACCESSION	U73583										
NID	g1657983										
SOURCE	German cockroach.										
ORGANISM	Blattella germanica										
Eukaryotes; mitochondrial eukaryotes; Metazoa; Arthropoda;											
Tracheata; Hexapoda; Insecta; Pterygota; Orthopteroidea; Blattaria;											
Blattellidae; Blattelinae; Blattella.											
REFERENCE	Dong, K.										
AUTHORS	1 (bases 1 to 6096)										
TITLE	A single amino acid change in the para sodium channel protein is associated with knockdown-resistance (kdr) to pyrethroid insecticides in German cockroach										
JOURNAL	Insect Biochem. Mol. Biol.	27 (2),	93-100	(1997)							
MEDLINE	97218696										
REFERENCE	2 (bases 1 to 6096)										
AUTHORS	Dong, K.										
TITLE	Direct Submission										
JOURNAL	Submitted (07-OCT-1996)	Entomology, Michigan State University, East Lansing, MI 48824, USA									
<hr/>											
FEATURES	Location/Qualifiers										
source	1..6096 /organism="Blattella germanica"										
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QY 1770 GCGCGCTT--TGSTAT-ACCGGAGGAGTCTGTAAGCCATTGGTATTGTCAACATATCAG 1826  
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QY 1827 GATGCCAGCAGCATTTGGCCCTATATGCCGACGACTCGAATGCCGTACACCCGATGTCGGAA 1886  
Db 1807 GAGAAATGGAGCAATAGTTGTACCAAGTTTATACGCCAGCCCTCGGTTTCAGGACCATCATCC 1866  
QY 1887 GAGAAATGGGCGCATATAGTCCGCGTGTACTATATGCAATCTTAGCTCCCGACACATCATCG 1946  
Db 1867 TATACATCACACGATCCAGGATATCTTACACGTCCTCATGGGACCTCCCTGGGTC-CA-G 1924  
QY 1947 TATACCTCGCATAGTCCGGAATATCGTATACCTCACTAGGCGATCTACTCGGCGGCGATG 2006  
Db 1925 GCAA-CRAAT-C-TCAGACCAA-GATCAATCA-A-C-----TGCGAGGTCTGTTCACTGCGC 1974  
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Db 1975 AA-CAACCCIT------CAC--A-GGTG-C-CTAA-T-TCT--ACACATACATGAATGC 2018  
QY 2067 AATCAATCAGTGGCGCCACCAATATGGGCGCACCACTGTCTGGACACCAATCACAAGCTC 2126  
Db 2019 G-TCAGCA-GAC-A-GTGAT--GA-TGAG----CGGT-GAAA--GCAA-AGCA--CA- 2059  
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QY 2427 TGGTGTGGTTGAAATTCAGGAGTGGGTATCGCTCATCTGCTTTCGATCCCTTCTGTCGAG 2486  
Db 2356 TTGTTTCACTACCCCTTTCGATTTGCTCAATACACTGTTATGCGCCCTCGACCCACGAC 2415  
QY 2487 CTCTTCACTACGCTGTGCTATTTGGTCAACAGATGTTTTCATGGCAATGGATCAACCGAT 2546  
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QY 2667 TGGAACTATCTCGACTTCATTTATCGTGGCCCTATCGCTATTTGGAACCTGGGACTCGAGGT 2726  
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Db 2716 AACTGTACCTTTGTGCTTGTGATATCATTTTTCATCTTTGCGGTCATGGGTATGCAACTC 2775  
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QY 3806 CATT-ATTATGACACAGCAGGAGGATATCTCGATGAATATCCAGCTGATTGCTGCCCG 3864  
Db 3704 ATCACTGTCTAAGCCGTTCCCTTCTTCTGCTGGAGACGAAAGACTCTCTCTTTCTGCGAAG 3763  
QY 3865 ATTCGACTATAAGAAATTTCCGATCTTAGCCGCTGACGATGACTCGCCGCTTTCTGCAAG 3924  
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[illegible]





Qy	2977	
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MEDLINE	96397510	
REFERENCE	2 (bases 1 to 5068)	
AUTHORS	Miyazaki, M., Ohshima, K., Dunlap, D.Y. and Matsumura, F.	
TITLE	Direct Submission	
JOURNAL	Submitted (17-SEP-1996) Environmental Toxicology, University of	
	California at Davis/ITEH, Davis, CA 95616, USA	
FEATURES	Location/Qualifiers	
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BASE COUNT	1363 a 1104 c 1252 g 1349 t	
ORIGIN		
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	Best Local Similarity 70.4%; Pred. No. 0.00e+00;	
	Matches 3659; Conservative 0; Mismatches 1402; Indels 136; Gaps 81;	
Db	1	CGCTGGAACTGGCTGGACTTCGTAGTAATAAGCTTTAGCTTACCTAAGTATGGGATAGAT 60
Qy	660	GCATGGAATTTGGCTGGACTTCGTAGTAATAAGCTTTAGCTTACCTAAGTATGGGATAGAT 719
Db	61	CTAGGAACCTGGCCGCTTGCAGACGTTCCAGGCTGCTCCGAGCTTTGAAGACTGTCGCT 120
Qy	720	TTAGGTAACTAGCAGCCCTTGCAGACGCTTTAGGGTGTCTGCGAGCGCTTAAACCCGTAGCG 779
Db	121	ATTCTTCCAGCTTTGAAGACCATTTGTGGCGCTGTGATTGAATCTGTAAAGAACCTGCGC 180
Qy	780	ATTCTGCGGCTTGAAGACCATTCGTGCGCGCTCATCATCAATCGGTGAAGAACTCTGCGC 839
Db	181	GATGTGATAATCTCACCATTGTTCTCGCTTCGCTTCGCTTAAATGGGCTCCAGATT 240
Qy	840	GATGTGATAATCTCACCATTGTTCTCGCTTCGCTTCGCTTAAATGGGCTCCAGATT 899
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Qy	900	TATATGGCGTGTCTACCCGAGAAGTGCAACAAGAAGTTCCCGCTGGACAGGTTCTCTGGGC	959
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Qy	960	AATCTGACCACGAGAACTGGGACTATCACATCCGATAGCTCCAATGGTATCCGAG	1019
Db	361	GAAGGTGCCACAGAAGTTCACATGTGTGGGAATTCATCAGGAGCTGGTACATGTCCACCT	420
Qy	1020	GACGAGGGCATCTCATTTCCGTTATTCGGCAATATATCCGTTGGGGGCGCAATGCGACGAC	1079
Db	421	GTATACACATGTCTCCAGSGCTTTGAGAAAATCCAACTATGTTACACCAAGTTTCGAT	480
Qy	1080	GATTACGTGTCCCTGCAGGGGTTTGTCCGAATCCGAATATGGCTACACCAAGCTTCGAT	1139
Db	481	ACGTTTTGTTGGGCATTCCTCTCGGCCCTTCAGACTGTAGCACCAGGATTAATGGGAGAAC	540
Qy	1140	TCGTTGCGATGGCTTTCCTGTCCGCCCTCCCGCTGTATGACACAGGACTCTCTGGAGGAT	1199
Db	541	CTTTATCAGCTGGTTTGTAGATCTGCTGGGCCCTGGCATACTGCTGTCTTCAATGTCTATC	600
Qy	1200	CTGTACCAGCTGGTTGTGGCGCGCGGACCATTGGCACATGCTGTTCTTTATAGTCATC	1259
Db	601	ATCTTCTTAGGCTCANTCTATCTTGTGAACCTTGATTTTGGCCATTGTCCCAATGCTCTAC	660
Qy	1260	ATCTTCTTAGGTTCAATCTATCTGTGAAATTTGATTTTGGCCATTGTTGCCATGCTGAT	1319
Db	661	GATGAGTTGCAGAGAAGCTGAGGAGGAAGACGACGGGAAGAGAGCGTTGAGGGA	720
Qy	1320	GACGAATGCAAGGAAGCGCCGAAGAAGAGGCTGCCGAAGAGGAGCGCATACGTGAA	1379
Db	721	CGGGAAGAAGCAGCTCTTCGGAAGAGGCGAAAAAATTAAGACAAAGCGGATAAACTGGC	779
Qy	1380	CGGGAAGAAGCTCGCCGCCCAAAGCGCCAACTGGAGGAGCGGCCAATGCCAGGCT	1439
Db	780	-AG-CACAGAANAATTACGACGACCAAGAACCTAGCTGGCGCAATCTAGCAAAAATCTCCC	837
Qy	1440	CAGCAGCAGCGGATCGGGCTCGCCGCAAGAGGCTGCACCTCGGAAATGGCCAAAG	1499
Db	838	TCGG-GAAGT-TCGTCTCGT-AGTTATGAGTTGTTTATAAATCAAAAGGACGCAATAAT	894
Qy	1500	AGTCCGAGCTATTCTTGCACTACGCTATAGACTATTGTTGGGGGGGAGAAGGGCAAGAT	1559
Db	895	GACAACAAAAGGAGAACATGAGCATCCGACGCA--AGGCGG---GGACTCGATAAGC	948
Qy	1560	GACAACAACAAGAGAAGATGTCCATTCGAGCGCTCGAGGTGGAGTCGGAGTCGCTGAC	1619
Db	949	GA-ACACAAGG-AAG-AGTGGGTCAAAATGTT-ACG--GGATCA--G---G-AAAGTG	996
Qy	1620	GTTATACAAAGACAACGACGACCTACCAAGACACACCAAGCTACCAAAAGTTTCGTAAGTG	1679
Db	997	AGCGCGCAACTTTGAGTCTACCGAGCTCACCTTTCACCATCGCCGAGGTTCCCAAGT	1056
Qy	1680	AGCAGACATCCCTTATCCTTACCTGGTTACCGTTTACCGTTTACATACGCGAGGGATCAGTAGT	1739
Db	1057	AGTCATCACTTTACAATTGAAACGGACGCTGGAAGGTTCTGTGGGCCACCTTGGTGGTAT	1116
Qy	1740	TC TCACAAGTACAGTACGGAACGGACGCTGCCCGCTT--TGGTAT-ACCCGGTAGCGAT	1796
Db	1117	CGAAAAACCCCTAGTACTTTCTAGTACCTTCGATGATGACCAAGAACATCTTCCTTATGACAGAT	1176
Qy	1797	CGTAAGCCATTGTTATGTTCAACATATCAGGATGCCAGCAGCACTTCCCTATGCGGCAC	1856
Db	1177	GACTCGAATCGATPACACCTTGTCTAGAGGAGAATGGNGCAATAGTTGTACCAAGTTTAT	1236
Qy	1857	GACTCGAATCCGCTACCCCGATGTTCCGAAGAGAATGGGGCCATCATAGTCCCGCTGAC	1916
Db	1237	TACGCCAGCCTCGGTTCCAGGCACTCATCCTATACATCACAGCAATCCAGGATATCTCTAC	1296
Qy	1917	TATGGCAATCTAGGCTCCGACACTCATCGTATACCTCGCATCAGTCCCGAATATCGTAT	1976
Db	1297	ACGTCTCATGGGACCTCTCTGGGTG-CA-GGCAA-CAAAAT-C-TCAGACCAA-GATCAAT	1350

Qy	1977	ACCTCACAATGGCGATCTACTCGCGCGCATGCGCGGCTCATGCGCGCTCAGCACAATATGACCAAG	20303
Db	1351	CA-A-C-----TGCAGTCCGTTTCAGTGGGCAA-CAACCCCTT-----CAC--A--GGTG-C	13993
Qy	2037	GAGAGCAATTGGCGAACCGCAACACACAGCAATCAATCAGTGGCGCGCCACCAATGGCGGC	2096
Db	1394	-CTAA-T-TCT--ACACCATACATGAATGGG-TCAGCA-GAC-A-GTGAT--GA-TGGAG	1441
Qy	2097	ACCACCTGTCTGGACACCAATCACAAAGTTCGATCATCGCACTACGAAATTGGCGCTGGAG	2156
Db	1442	----CGGT-GAAA--GCAA-AGCA--CA-C-TGACATCCATTCATTGACAAATGCAG	1488
Qy	2157	TGCAGCGACGAGCTGGCAAGATTAAACATCATGACAATCCTTTATCGAGCCGCTCAG	2216
Db	1489	CAAACTACAAATCTTGATATGAATGATGAATGTGCTGGAATGACATATATAGAACAAAGCT	1548
Qy	2217	ACACAACGGTGTTCATATGAAGATGTGATGGTCTTGATGACATCATCGRACAGGCC	2276
Db	1549	GCTGGACGACAGATAGCCAGTGAACATGGAGACGAAAGATGACGAGGCTTCCAAACAGTT	1608
Qy	2277	GCTGGTCGACAGTGGGCAAGCGATCGCGTGTCTCCGTTTACTATTTCCTCCCAACAGAG	2336
Db	1609	AAAGA-CA--AGG-TG-----TT-----AG-CTAT--A-T-----GT-ATGCG---AGGT	1641
Qy	2337	GACATGACGAGATGGCGACGCTTCAAGACAAGGCATCGAAGTGAATCCTCAAGGC	2396
Db	1642	ATCGACATCTTCGCGTGGGATGTTGCTGGCTCTGGCTCAAGTCCAAAGATACGTC	1701
Qy	2397	ATCGATGTGTTTGTGTGGGACTGTGCTGGGTTGGTTGNAATTTCAAGAGTGGGTA	2456
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Qy	2517	ACGATGTTTCATGGCAATGATCACCACGATATGAACAAGGAGATGGAACGCGTCTCAAG	2576
Db	1822	AGTGGCAACTATTTCATCAGCGACCTTTGCGATTGAGCGACGCTCAAGTTGATAGCA	1881
Qy	2577	AGTGGCAACTATTTCATCCCGCCACCTTTGCCATCGAGGCCACCATGAAGCTAATGGCC	2636
Db	1882	ATGAGCCCTAAGTACTACTTCCAGGAAGSATGGAACATTTTTGATTTTCATCATTTGTGCA	1941
Qy	2637	ATGAGCCCAAGTACTATTTCAGGAGGCTTGAACATCTTCGACTTCATTTCTGTCGCC	2696
Db	1942	CTTTCTCTGCTGGAATTGGTCTTGAAGTGTCCAAGTGTCTCGCTGCTGCGATCGTTC	2001
Qy	2697	CTATCGTATTTGGAATGGGACTCGAGGCTGTCAAGGCTCTCCGCTATTTCGCTTCCTT	2756
Db	2002	AGATTGTTGAGAGTCTTCAAACCTTCGGAAGTCTTGGCCGACGCTGAATCTGCTCATTTCC	2061
Qy	2757	CGATTGCTGGTGTATTAACATTGGCCAAGTCTTGCCCAACATTAATTTACTCATTTTCG	2816
Db	2062	ATCATGGGTAGAACTCTTGCTCTGGGTAACTCGACTTTGCTCTTTGTTATTATTCATT	2121
Qy	2817	ATTATGGACGCACCATGGSCCTTTGGGTATCTGACATTTGACTTTGCATTATCATC	2876
Db	2122	TTCACTTTTCCGCTATGGGTATGCAACTCTTTTGGCAAAAATTAATATGATAATTTGTAA	2181
Qy	2877	TTCATCTTTCCGGTGTATGGGAATGCAACTGTTTCGGAAAGAAATTTATCATGACACAAGAC	2936
Db	2182	CGTTTCCCTCACGGGATATGCCGAGATGGAACCTTACGGACTTCATGCACTCATTTCATG	2241
Qy	2937	CGCTTTCCGATGGCACTTGGCGGCTTGAACCTTTCACCGACTTTATGACAGACTTCATG	2996
Db	2242	ATTGTTTCCGAGTGTGTGTGGAGAGTGGATAGAGTCTATGTGGGATTTGTATCTTGTT	2301
Qy	2997	ATCTGTTCGCGGTGCTCTCGGAGANAATGGATCGAATCCATGTGGGACTGCATGTACCTG	3056
Db	2302	GGAGACTGTGCTGCATCCCGTTCTTTTGGCCACTGTGCTCATTGGAAAATTTGGTTGTG	2361
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ORGANISM Drosophila melanogaster  
Eukaryotes; mitochondrial eukaryotes; Metazoa; Arthropoda;  
Tracheata; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.  
REFERENCE 1 (bases 1 to 1840)  
AUTHORS Thackeray,J.R. and Ganetzky,B.  
TITLE Developmentally regulated alternative splicing generates a complex array of Drosophila para sodium channel isoforms  
J. Neurosci. 14 (5 Pt 1), 2569-2578 (1994)  
JOURNAL 94238327  
MEDLINE 2 (bases 1 to 1840)  
REFERENCE Thackeray,J.R. and Ganetzky,B.  
AUTHORS Conserved alternative splicing patterns and splicing signals in the Drosophila sodium channel gene para  
TITLE Genetics 141 (1), 203-214 (1995)  
JOURNAL 96042905  
MEDLINE 3 (bases 1 to 1840)  
REFERENCE Thackeray,J.R. and Ganetzky,B.  
AUTHORS Direct Submission  
TITLE Submitted (10-MAY-1995) Justin R. Thackeray, Biology, Yale University, 266 Whitney Avenue, New Haven, CT 06520, USA  
JOURNAL Location/Qualifiers  
FEATURES  
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alternatively spliced, partial cds.  
ACCESSION UB3871  
NID 92231544  
KEYWORDS horn fly.  
SOURCE Haematobia irritans  
ORGANISM Eukaryotes; mitochondrial eukaryotes; Metazoa; Arthropoda;  
Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera;  
Muscomorpha; Muscoidea; Muscidae; Haematobia.  
REFERENCE 1 (bases 1 to 947)  
AUTHORS Guerrero,F.D., Jamroz,R.C., Kammlah,D. and Kunz,S.E.  
TITLE Toxicological and molecular characterization of  
pyrethroid-resistant horn flies, Haematobia irritans:  
identification of kdr and super-kdr point mutations  
Insect Biochem. Mol. Biol. 27 (8-9), 745-755 (1997)  
JOURNAL 98105586  
MEDLINE 2 (bases 1 to 947)  
REFERENCE Guerrero,F.D., Jamroz,R.C. and Kunz,S.E.  
AUTHORS Direct Submission  
TITLE Submitted (06-JAN-1997) USDA-ARS, Knippling-Bushland Livestock  
JOURNAL Insects Research Laboratory, 2700 Fredericksburg Road, Kerrville,  
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MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Sun Sep 13 07:20:22 1998; Maspar time 249.45 seconds  
1217.927 Million cell updates/sec  
Tabular output not generated.

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Title:
Description:
Perfect Score:
N. A. Sequence:
Comp:

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Scoring table: TABLE default  
Gap 6

Nmatch STD : Dbase 0: Query 0

Searched: 88822 seqs, 23323279 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: n-issued  
1:5\_COMB 2:PCT9\_COMB 3:backfiles1

Statistics: Mean 10.185; Variance 5.490; scale 1.855

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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	2	6513	100.0	6513	1	US-08-337-	Sequence 7	Applicatio	0.00e+00
	3	6513	100.0	6513	1	US-08-724-	Sequence 7	Applicatio	0.00e+00
	4	6513	100.0	6513	1	US-08-338-	Sequence 7	Applicatio	0.00e+00
	5	6513	100.0	6513	2	PCT-US95-1	Sequence 7	Applicatio	0.00e+00
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	8	41	0.6	215	1	US-08-238-	Sequence 5	Applicatio	2.09e-10
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Db 4561 CGTATCTGTCCCTTTTCCAAAGTGGCCACCTTCAAAGCTGGATACAAATCATGAACGATG 4620  
QY 4561 CGTATCTGTCCCTTTTCCAAAGTGGCCACCTTCAAAGCTGGATACAAATCATGAACGATG 4620  
Db 4621 CTATCGAATCAGAGAGTGGACAAAGCAATTCGTGAAGCAATCTACATGATTT 4680  
QY 4621 CTATCGAATCAGAGAGTGGACAAAGCAATTCGTGAAGCAATCTACATGATTT 4680  
Db 4681 TATATTCGATTTCTCATCATATTTGGATCCCTTTTACACTCAATCTGTTCAATGGTG 4740  
QY 4681 TATATTCGATTTCTCATCATATTTGGATCCCTTTTACACTCAATCTGTTCAATGGTG 4740  
Db 4741 TTATCATTTGATAATTTTATGAGCAAAAGAAAAGCAAGTGGATCATTAGAATGTTCA 4800  
QY 4741 TTATCATTTGATAATTTTATGAGCAAAAGAAAAGCAAGTGGATCATTAGAATGTTCA 4800  
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QY 4801 TGACAGAAAGTACAGAAAGTACTATATCTGATGAAAGATGGCTCTTAAAGAACCAT 4860  
Db 4861 TAAAGCCATTCCAAAGACCAAGTGGCGACCAAGCAATAGTCTTGAATAGTAAACG 4920  
QY 4861 TAAAGCCATTCCAAAGACCAAGTGGCGACCAAGCAATAGTCTTGAATAGTAAACG 4920  
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QY 4921 ATAAGAAATTCGATATAATCATTAATGATTTATTCATTTGCTGTAACATGATGACCC 4980  
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QY 4981 TCGATCGTACGATCGCTCGGACACGTATACGCGCTCTAGACTATCTCAATGCCATAT 5040  
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QY 5041 TCGTAGTTATTTTCAGTTCCGAATGTCTATTAATAATATTTCGCTTTACGATATCACTATT 5100  
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QY 5161 TACTTAGCGATATTATCAGAAAGTACTTCGTGTCGCGACCCCTGCTCCGAGTGGTGGTG 5220  
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QY 5221 TGGCGAAAGTGGGCGGTGTCCTTCGACTGTTGAAAGGAGCCAAAGGATTCGGACATGC 5280  
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QY 5281 TCTTCGCGTGGCCATGTCGTCGCGGCCCTGTTCAACATCTGCTGCTGTTCTCTGG 5340  
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Db 5401 GCATTAAACGACGTCTACAACCTTCAAGACCTTTGGCCAGAGCATGATCTCTGCTCTTTTCA 5460  
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QY 5461 TGTGCGAGTCAAGCGGTTGGGATGTTGACTTGACGCCATTTATCAATGAGGAAGCATGCG 5520  
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QY 5581 CGTTTCTCTCTCATACCTAGTTTATAAGCTTTTGTAGTATTAATATGATGATGCTG 5640  
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QY 5641 TCATTCTCGAAGACTATAGTCAGGCCACCCAGGACGTCGAAGAGGTCGAACGAGCAG 5700  
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QY 5701 ACTAGCATGTACTATGAGATCTGCGAGCAATTCGATCCGAGGGCACCAGTACATAC 5760  
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QY 5821 CGAACAGTCAAGATCATATCGATGACATACCCATCTGTGCGGGTGAACCTCATGTACT 5880  
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QY 5941 AGGAGCGGTTGAGATTGGTGAGATAGCGGCCCGCCGGATACGGAGGCTACGAGCCCG 6000  
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QY 6001 TCTCATCAACGCTGTGCGGTGAGAGTACTGCGCCCGCTATTCAGCACACGCT 6060  
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QY 6121 GCGATGGCGGTGATCCGATGCGGGGACCGCGCCCGATGAAGCAACGACGCGCATG 6180  
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QY 6241 AGAGTAAATGTAATAGTCCGGGTGAGGATGACGCGCGCGGATGAGAGAGGAGTCCGATG 6300  
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QY 6301 CGCGCGCGCGGACAGCAGCGCGGGAAGTCCCGGAGCGGGTAGCGCCGGGCGACAGA 6360  
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Db 6481 CCTCTCAAGATGACGCGAGTATTAGCTCTAGA 6513  
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RESULT 2  
ID US-08-337-339-7 STANDARD; DNA; UNC; 6513 BP.  
AC xxxxxx  
DT  
DE Sequence 7, Application US/08337339  
CC Sequence 7, Application US/08337339  
CC Patent No. 5593864  
CC GENERAL INFORMATION:  
CC APPLICANT: Warmke, Jeffrey W.  
CC APPLICANT: Hall, Linda  
CC APPLICANT: Feng, Gouping  
CC APPLICANT: Van Der Ploeg, Leonardus  
CC TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE  
CC TITLE OF INVENTION: PARA SODIUM CHANNEL  
CC NUMBER OF SEQUENCES: 7  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: John W. Wallen III  
CC STREET: P.O. Box 2000, 126 E. Lincoln Avenue  
CC CITY: Rahway  
CC STATE: New Jersey  
CC COUNTRY: USA  
CC ZIP: 07065-0900  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: PatentIn Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/337,339  
CC FILING DATE:  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Wallen III, John W.  
CC REGISTRATION NUMBER: 35,403  
CC REFERENCE/DOCKET NUMBER: 19332  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (908) 594-3905  
CC TELEFAX: (908) 594-4720  
CC INFORMATION FOR SEQ ID NO: 7:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 6513 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: cDNA  
CC SEQUENCE 6513 BP; 1661 A; 1548 C; 1702 G; 1582 T; 0 OTHER.

Query Match 100.0%; Score 6513; DB 1; Length 6513;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 TCTAGACGTTGGCCGATAGACAATGACAGAAGATTCGACTCGATATCTGAGGAAGAAC 60  
QY 1 TCTAGACGTTGGCCGATAGACAATGACAGAAGATTCGACTCGATATCTGAGGAAGAAC 60

Db 61 GCAGTTTGTTCGTCCTTACCCCGCAATCATTTGGTCAATCGAAACGCAATGCGG 120  
QY 61 GCAGTTTGTTCGTCCTTACCCCGCAATCATTTGGTCAATCGAAACGCAATGCGG 120

Db 121 CTGAACATGAAAGCAGAGGAGCTGGAAGAAAGAGAGCCGAGGAGAGTGCGCGCAT 180  
QY 121 CTGAACATGAAAGCAGAGGAGCTGGAAGAAAGAGAGCCGAGGAGAGTGCGCGCAT 180

Db 181 ATGTGCGCAAGAAAAACAAAAAGAAATCCGATATGATGACGAGGACGAGGATGAAGTGC 240  
QY 181 ATGTGCGCAAGAAAAACAAAAAGAAATCCGATATGATGACGAGGACGAGGATGAAGTGC 240

Db 241 CACACCCGGATCCTACATCTGACAGGGGTGCGCAATACCTGTCGATTGCGAGGCGAGCT 300

QY 241 CACACCCGGATCCTACATCTGACAGGGGTGCGCAATACCTGTCGATTGCGAGGCGAGCT 300  
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QY 301 TCCCGCGGGAATGGCCTCCACTCCTCTCGAGGATATCGATCCCTACTACAGCAATGTAC 360  
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QY 421 TGTGATGCTCGATCCATTCATCCGATAGCTGCTGTTGGCCATTACATTTCTAGTGCATC 480  
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QY 481 CATTATTTTCCCTATTTCATCATCAACCAATTCCTCGTCAACTGCTGATGATAATGC 540  
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QY 541 CGACAAGCCACCGTTGAGTCCACTGAGTGTATATTCACCGGAATCTACACATTTGAAT 600  
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QY 721 TAGTAATCTAGCAGCCCTGCGAAGCTTTAGGGTCTGCGAGCGCTTAAACACCGTAGCCA 780  
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QY 781 TTGTGCCAGGCTTGAAGACCATCTGCGCGCCGTCATCGAATCGGTGAAGAAATCTGCGCG 840  
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QY 841 ATGTGATTATCTGACCATGTTCTCCCTGTCGGTGTTCGGCTTCATGGCTCAGATCT 900  
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QY 961 ATCTGACGAGGAACTGGGACTATCACATCCCAATAGCTCCCAATGTTATTCGAGG 1020  
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QY 1021 ACAGGGCATCTCATTTCCGTTATCGGCAATATATCCGGTGGGGCAATGCGACGACG 1080  
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QY 1081 ATTACGTTGCTCGAGGGTTTGGTCCGAATCCGAATATGCTACACAGCTTCGATT 1140  
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QY 1141 CGTTCGATGGCTTTCCTGTCGCCCTTCGGCTGATGACACAGACTTCTGAGGAGATC 1200  
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QY 1201 TGTACAGCTGCTGTCGCGCCCGGACCATGGACATGCTCTTTCTTATAGTCATCA 1260  
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QY 1381 CGGAAGAACTCGCGCGCCGAAGCGGCAAGCTGAGAGAGGCGGCCAATGCGCAGGCTC 1440  
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Db 1621 TTATACAAAGACAACAGCAGCACTACACAGCAGCAGCACTACCAAGTTCTGTAAGTGA 1680  
QY 1621 TTATACAAAGACAACAGCAGCACTACACAGCAGCAGCACTACCAAGTTCTGTAAGTGA 1680  
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Db 1801 AGCCATTGGTATTGTCAACATATCAGGATGCCAGCAGCACATTGCCCTATGCCGAGACT 1860  
QY 1801 AGCCATTGGTATTGTCAACATATCAGGATGCCAGCAGCACATTGCCCTATGCCGAGACT 1860  
Db 1861 CGAATCCGCTACCCCGATGTCGGAAGAAATGGGCCATCATAGTCCCGTGTACTATG 1920  
QY 1861 CGAATCCGCTACCCCGATGTCGGAAGAAATGGGCCATCATAGTCCCGTGTACTATG 1920  
Db 1921 GCAATCTAGGCTCCCGACACTCATCGTATACCTCGCATCAGTCCCGAATATCGTATACCT 1980  
QY 1921 GCAATCTAGGCTCCCGACACTCATCGTATACCTCGCATCAGTCCCGAATATCGTATACCT 1980  
Db 1981 CACATGGCGATCTACTCGGCGCATGGCGTATGCGGCTCAGCACAATGACCAAGGAGA 2040  
QY 1981 CACATGGCGATCTACTCGGCGCATGGCGTATGCGGCTCAGCACAATGACCAAGGAGA 2040  
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QY 2041 GCAAAATTGGCAACCCGAACACACAGCAATCAATCAGTGGCGCCACCAATGGCGGACCA 2100  
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QY 2221 AAACGGTGGTGTATGAAGATGTGATGGTCTGAATGACATCATCGAAGAGCGCGCTG 2280  
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Db 2461 TCATCGTCTTCGATCCCTTCGTCGAGCTCTTCATCACGCTGTGCATTGTGTCAACAGA 2520  
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QY 2521 TGTTCATGGCAATGGATCACCACGATATGAACAAGGAGATGAACGCGTGTCAAGAGTG 2580  
Db 2581 GCAACTATTTCTTACCAGCCACCTTTGGCATCGAGGCCACCATGAAGCTAATGGCCATGA 2640  
QY 2581 GCAACTATTTCTTACCAGCCACCTTTGGCATCGAGGCCACCATGAAGCTAATGGCCATGA 2640  
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QY 2701 CGCTATTGGAATCGGACTCGAGGCTGTCAGGGTCTCTCGTATTCGTTCCCTTCGAT 2760  
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QY 2881 TCTTTGCGGTGATGGGAATGCAACTGTTTCGGAAGAATATCATGATCACAAGGACCGCT 2940  
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QY 2941 TTCGGATGGCGACCTGCGCGCTGGAACTTCACCGACTTTATGCGACAGCTTCATGATCG 3000  
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QY 3001 TGTTCGCGGTGCTCTGCGGAGAATGGATCGAGTCCATGCGGACTGCACTGACGTTGGGCG 3060  
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QY 3181 CGGATAACGATACGAATAAATAGCCGAGGCTTCAATCGAATTGGCCGATTTAAAAAGTT 3240  
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Db 3421 AGGGATCAAGGAGCAGACGCAACTGGAGTGGCCATCGGGATCGGATGGAATTCAGA 3480  
QY 3421 AGGGATCAAGGAGCAGACGCAACTGGAGTGGCCATCGGGATCGGATGGAATTCAGA 3480  
Db 3481 TACACGGGACATGAAGAACAAACAGGAGGAGAAATCCAAATATCTAAATACGCAAGA 3540  
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D	b	3541	TGATTGGCAACTCAATTAACCAACCAAGACATAGACTGGAAACAGAGCTAAACCATAGAG	3560
Q	y	3541	TGATTGGCAACTCAATTAACCAACCAAGACATAGACTGGAAACAGAGCTAAACCATAGAG	3560
D	b	3601	GTTTGTCTTTACAGGACGACGACACTGCCAGCATTAACCTCATATGTTAGCCATAAGAATC	3660
Q	y	3601	GTTTGTCTTTACAGGACGACGACACTGCCAGCATTAACCTCATATGTTAGCCATAAGAATC	3660
D	b	3661	GACCATTTCAAGACGAGAGCCCAAGAGGCGCGGAGACGATGGAGGGCGAGGAAGC	3720
Q	y	3661	GACCATTTCAAGACGAGAGCCCAAGAGGCGCGGAGACGATGGAGGGCGAGGAAGC	3720
D	b	3721	CGACGCCAGCAAGAGGAGATTAGTCTCGACGAGGAACCTGGACGAGAGGGCGAATGCG	3780
Q	y	3721	CGACGCCAGCAAGAGGAGATTAGTCTCGACGAGGAACCTGGACGAGAGGGCGAATGCG	3780
D	b	3781	AGGAGGGCCGCTCGACGGTGATATCATTTATTCACACGACGAGGATATCTCGATG	3840
Q	y	3781	AGGAGGGCCGCTCGACGGTGATATCATTTATTCACACGACGAGGATATCTCGATG	3840
D	b	3841	AATATCCAGCTGATTGCTGCCCGGATTGCTACTATAAGAAATTTCCGATCTTAGCCGGTG	3900
Q	y	3841	AATATCCAGCTGATTGCTGCCCGGATTGCTACTATAAGAAATTTCCGATCTTAGCCGGTG	3900
D	b	3901	ACGATGACTCGCGGTTCTGCAAGGATGGGCAATTTACGACTGAAATCTTTCAATTA	3960
Q	y	3901	ACGATGACTCGCGGTTCTGCAAGGATGGGCAATTTACGACTGAAATCTTTCAATTA	3960
D	b	3961	TTGAAATAAATATTTTGAACAGCTGTTATCACHATCATGATTTTAAATGAGTAGCTTAGCTT	4020
Q	y	3961	TTGAAATAAATATTTTGAACAGCTGTTATCACHATCATGATTTTAAATGAGTAGCTTAGCTT	4020
D	b	4021	TGGCATTAGAAGATGTACATCTGCCACAAGACCCACTACTCGACGATATTTTATACTATA	4080
Q	y	4021	TGGCATTAGAAGATGTACATCTGCCACAAGACCCACTACTCGACGATATTTTATACTATA	4080
D	b	4081	TGGACAGAATATTTACGGTTATATCTCTTGGAAATGTTAATCAAGTGGTTGGCGCTCG	4140
Q	y	4081	TGGACAGAATATTTACGGTTATATCTCTTGGAAATGTTAATCAAGTGGTTGGCGCTCG	4140
D	b	4141	GCITCAAGTGTACTTTCACCAACGGTGGTGTGGCTCGATTTGCTGATTTGTCATGGTAT	4200
Q	y	4141	GCITCAAGTGTACTTTCACCAACGGTGGTGTGGCTCGATTTGCTGATTTGTCATGGTAT	4200
D	b	4201	CGCTTATCAACTTCGTTGCTTCACTTTGTTGGAGCTGGTGTTATTCAGCCCTTCAAGACTA	4260
Q	y	4201	CGCTTATCAACTTCGTTGCTTCACTTTGTTGGAGCTGGTGTTATTCAGCCCTTCAAGACTA	4260
D	b	4261	TGCGAAGCTTTAAGAGCACTGAGACCACTACGTGCCATGTCCCGTATGCAGGCATGAGGG	4320
Q	y	4261	TGCGAAGCTTTAAGAGCACTGAGACCACTACGTGCCATGTCCCGTATGCAGGCATGAGGG	4320
D	b	4321	TCGTGCTTAATGGCGTGGTACAAGCTATACCGTCCATCTTCAATGTGCTATTTGGTGTGTC	4380
Q	y	4321	TCGTGCTTAATGGCGTGGTACAAGCTATACCGTCCATCTTCAATGTGCTATTTGGTGTGTC	4380
D	b	4381	TAATATTTTGGCTAAATTTTGGCCATAATCGSGTGTAACGCTTTTTCGTGGAAAAATTTT	4440
Q	y	4381	TAATATTTTGGCTAAATTTTGGCCATAATCGSGTGTAACGCTTTTTCGTGGAAAAATTTT	4440
D	b	4441	AGTCGAGGACATGAATGGCCAGAAAGCTCAGCCAGAGATCATACCAATCGCAATGCCT	4500
Q	y	4441	AGTCGAGGACATGAATGGCCAGAAAGCTCAGCCAGAGATCATACCAATCGCAATGCCT	4500
D	b	4501	CGGAGCGGAGAACTACACGTGGTGAATTCAGAAATGAATTTGATCATGTAGGTAAAG	4560
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D	b	4561	CGTATCTGTCCTTTTCCAGTGGCCACCTTCAAAGGCTGGATACAAATCATGACCAATG	4620
Q	y	4561	CGTATCTGTCCTTTTCCAGTGGCCACCTTCAAAGGCTGGATACAAATCATGACCAATG	4620
D	b	4621	CTATCGATTCCAGAGAGGTTGGACAAGCAACCAATTCGTGAAACGAACATCTACATGTATT	4680

[illegible]

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QY 5821 CGAACAGTACAGATCATATCGATGGACATACCCATCTGTCCGGGTGACCTCATGTACT 5880  
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QY 5881 GCGTCGACATCTCGACGCCCTTACGAAGACTTCTTTGCGGGAAGGCAATCCGATAG 5940  
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QY 5941 AGGAGACGGGTGAGATTGGTGAGATAGCGGCCCGCCGGATACGAGGGCTACGAGCCCG 6000  
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RESULT 3  
ID US-08-724-095-7 STANDARD; DNA; UNC; 6513 BP.  
AC xxxxxx

DE Sequence 7, Application US/08724095  
CC Sequence 7, Application US/08724095  
CC Patent No. 5688917

CC GENERAL INFORMATION:  
CC APPLICANT: Warmke, Jeffrey W.  
CC APPLICANT: Hall, Linda  
CC APPLICANT: Feng, Gouping  
CC APPLICANT: Van Der Ploeg, Leonardus  
CC TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE  
CC NUMBER OF INVENTION: PARA SODIUM CHANNEL  
CC TITLE OF SEQUENCES: 7  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: J. Mark Hand - Merck & Co., Inc.  
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CC CITY: Rahway  
CC STATE: New Jersey  
CC COUNTRY: USA  
CC ZIP: 07065-0907  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: FASTseq. Version #1.d5  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/724,095  
CC FILING DATE:  
CC CLASSIFICATION: 536  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Hand, J. Mark  
CC REGISTRATION NUMBER: 36,545  
CC REFERENCE/DOCKET NUMBER: 19332DA  
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CC INFORMATION FOR SEQ ID NO: 7:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 6513 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: cDNA  
CC SEQUENCE 6513 BP; 1681 A; 1548 C; 1702 G; 1582 T; 0 OTHER.  
  
Query Match 100.0%; Score 6513; DB 1; Length 6513;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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QY 1 TCTAGAGCTTGGCCGCGATAGACAATGACAGAAGATTCGGACTCGATATCTGAGGAAGAAC 60  
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QY 61 GCAGTTTGTTCGCTCCCTTTACCCGCGAATCATTTGGTGCAAATCGAAACACGCATTGCCG 120  
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QY 181 ATGTCGCAAGAAAAACAAAAAGAAATCCGATATGATGACGAGGACGAGGATCAAGGTC 240  
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QY 241 CACAACCGGATCCCTACACTTTGAACAGGGTGTGCCAATACCTGTTCGATTGCGAGGACGT 300  
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QY 1561 ACACACAAGAGAGATGTCATTCGGAGCGTCGAGGTGGAGTGGAGTGGGTGAGCG 1620  
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Db 4981 TCGATCGTTACGATGCGTCGACACGATATACGCGGTCCTAGACATATCTCAATCCGATAT 5040  
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Db 5221 TGGCGAAGTGGGCGCTGCTCCGCTGCTGAGTGAAGGAGCCAGGCAATTCGGACACTGC 5280  
QY 5221 TGGCGAAGTGGGCGCTGCTCCGCTGCTGAGTGAAGGAGCCAGGCAATTCGGACACTGC 5280  
Db 5281 TCTTCGCGTTGGCCATGTCGCTGCGGCGCTGTTCAACATCTGCCTGCTGCTTCCTGG 5340  
QY 5281 TCTTCGCGTTGGCCATGTCGCTGCGGCGCTGTTCAACATCTGCCTGCTGCTTCCTGG 5340  
Db 5341 TCATGTTCACTTTTCCGATTTTCGGCATGCTGTTTCATCGCAGCTGAAGAGAGAGCG 5400  
QY 5341 TCATGTTCACTTTTCCGATTTTCGGCATGCTGTTTCATCGCAGCTGAAGAGAGAGCG 5400  
Db 5401 GCATTACGAGCTCTACAACCTCAAGACCTTTGGCCAGAGCATGCTGCTCTTTTACA 5460  
QY 5401 GCATTACGAGCTCTACAACCTCAAGACCTTTGGCCAGAGCATGCTGCTCTTTTACA 5460  
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QY 5461 TGTCCAGCTACGCGGTTGGGATGGTGTACTGGACGCACTTATCAATGAGGAACATCGC 5520  
Db 5521 ATCCACCGCAGCAGCAAAAGGCTATCGGCAATTTGTGGTTCAGCAGCTTGGATATA 5580  
QY 5521 ATCCACCGCAGCAGCAAAAGGCTATCGGCAATTTGTGGTTCAGCAGCTTGGATATA 5580  
Db 5581 CGTTTCTCTCATACCTAGCTTATAGCTTTTGTAGTATTATTAATGTACATTCGCTG 5640  
QY 5581 CGTTTCTCTCATACCTAGCTTATAGCTTTTGTAGTATTATTAATGTACATTCGCTG 5640  
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QY 5641 TCATTCTCGAAGCTATAGTCAGGCGCCAGGAGCGTCAAGAGGGTCTAACCCAGCAGC 5700  
Db 5701 ACTACGACATGATATGAGATCTGGCAGCAATTCGATCCGGAGGCGCACCGATACATC 5760  
QY 5701 ACTACGACATGATATGAGATCTGGCAGCAATTCGATCCGGAGGCGCACCGATACATC 5760  
Db 5761 GCTATGATCAGCTGTCGAAATCTCTGACGCTACTGGAGCCCTGCTGAGCCCTGCTGATC 5820  
QY 5761 GCTATGATCAGCTGTCGAAATCTCTGACGCTACTGGAGCCCTGCTGAGCCCTGCTGATC 5820  
Db 5821 CGAACAAGTACAAGATCATATCGATGACATACCATCTGTCGCGGTCGACCTCATGTACT 5880  
QY 5821 CGAACAAGTACAAGATCATATCGATGACATACCATCTGTCGCGGTCGACCTCATGTACT 5880  
Db 5881 CGCTCGACATCCTCGACGCCCTTACGAAAGACTTCTTTGCGCGGAAGGCAATCCGATAG 5940  
QY 5881 CGCTCGACATCCTCGACGCCCTTACGAAAGACTTCTTTGCGCGGAAGGCAATCCGATAG 5940  
Db 5941 AGGAGAGGGTGAGATGGTGAGATAGCGGCCCGCCCGGATACGAGGGCTACGAGCCCG 6000  
QY 5941 AGGAGAGGGTGAGATGGTGAGATAGCGGCCCGCCCGGATACGAGGGCTACGAGCCCG 6000  
Db 6001 TCTCATCAACGCTGTGGCGTCAGGAGTACTGCGCCCGGCTAATCCAGCAGCGCT 6060  
QY 6001 TCTCATCAACGCTGTGGCGTCAGGAGTACTGCGCCCGGCTAATCCAGCAGCGCT 6060  
Db 6061 GCGGAAGCACAAGCGCGCGGAGGAGGTGGGTCTCTTTGAGCCGGATACGGATCATG 6120

QY 6061 GGGCAAAACGACAAAGCGCGCGGAGGAGGTGGTCTTTGAGCCGGATACGGATCATG 6120  
Db 6121 GCATGCGCGTGTATCCGATGTCGCGGACCCGCGCCGATGAAGCAACGAGCGCGCATG 6180  
QY 6121 GCATGCGCGTGTATCCGATGTCGCGGACCCGCGCGGATGAAGCAACGAGCGCGCATG 6180  
Db 6181 CGCCCGCTGTGGAGATGTTAGTGTAAACGCTACTGCAGAAAGAGCTGCCGATGCCGATG 6240  
QY 6181 CGCCCGCTGTGGAGATGTTAGTGTAAACGCTACTGCAGAAAGAGCTGCCGATGCCGATG 6240  
Db 6241 AGAGTAATGTAATAGTCCCGGTGAGGATCAGCGGCGGCGGAGCAGCAGCAGCAG 6300  
QY 6241 AGAGTAATGTAATAGTCCCGGTGAGGATCAGCGGCGGCGGAGCAGCAGCAGCAGCAG 6300  
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QY 6301 CGCGCGCGCGGCGCACGACGCGGGAAGTCCCGGAGCGGTAGCGCGGCGGAGCAG 6360  
Db 6361 CGCGCGTCTCTGGAGAGCAGCGGTTCTGTAGCAAGAACGCCCAAGGTGTCTATCC 6420  
QY 6361 CGCGCGTCTCTGGAGAGCAGCGGTTCTGTAGCAAGAACGCCCAAGGTGTCTATCC 6420  
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QY 6421 ACTCGGATCCGCGAGCATCAGTCCGCGCAGCGGCGGATGTCTGAGCCAGGCTCGCCCC 6480  
Db 6481 CCTCCAAGATGACGCGGAGTATTAGCTCTAGA 6513  
QY 6481 CCTCCAAGATGACGCGGAGTATTAGCTCTAGA 6513

## RESULT 4

ID US-08-338-702-7 STANDARD; DNA; UNC; 6513 BP.  
AC xxxxxx

DE Sequence 7, Application US/08338702  
CC Sequence 7, Application US/08338702  
CC Patent No. 5550049

## GENERAL INFORMATION:

CC APPLICANT: Warnke, Jeffrey W.

CC APPLICANT: Van Der Ploeg, Leonardus

CC TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE

CC TITLE OF INVENTION: PARA SODIUM CHANNEL

CC NUMBER OF SEQUENCES: 7

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: John W. Wallen III

CC STREET: P.O. Box 2000, 126 E. Lincoln Avenue

CC CITY: Rahway

CC STATE: New Jersey

CC COUNTRY: USA

CC ZIP: 07065-0900

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: PatentIn Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/338,702

CC FILING DATE:

CC CLASSIFICATION: 435

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Wallen III, John W.

CC REGISTRATION NUMBER: 35,403

CC REFERENCE/DOCKET NUMBER: 19338

CC TELECOMMUNICATION INFORMATION:

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CC TELEFAX: (908) 594-4720

CC INFORMATION FOR SEQ ID NO: 7:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 6513 base pairs

CC TYPE: nucleic acid

CC STRANDEDNESS: single

[illegible]



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QY 2101 CTTGTCTGGACACCAATCACAAGCTCGATCATCGGACTACGAAATTTGGCCTGGAGTGCA 2160  
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QY 2161 CGGACGAAGCTGCGAAGATTAACATCATCATCAATCTCTTTATTCGAGCCCGTCCAGAC 2220  
Db 2221 AAACGGTGGTGTATATAAAGATGTGTCTCTGTAATGACATCATCGAAGAGCCGCTG 2280  
QY 2221 AAACGGTGGTGTATATAAAGATGTGTCTCTGTAATGACATCATCGAAGAGCCGCTG 2280  
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QY 2281 GTCCGACAGTCGGGCAAGCGATCGCGGTGTCTCCGTTTACTATTTCCCAACAGAGACG 2340  
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QY 2401 ATGTGTTTCTGTGTGGACTGTGTCTGGGTGTGGTTTGAATTTTCAGGAGTGGGTATCGC 2460  
Db 2461 TCATCGTCTTCGATCCCTCGTGGAGCTCTTCATCGAGCTGTGCTATTCAGGAGTGGGTATCGC 2520  
QY 2461 TCATCGTCTTCGATCCCTCGTGGAGCTCTTCATCGAGCTGTGCTATTCAGGAGTGGGTATCGC 2520  
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QY 2581 GCAACTATTTCTCACCGCCACCTTTGCCATCGAGGCCACCATGAAGCTAATGCCATGA 2640  
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QY 2821 TGGGACCCACATGGCGCTTTGGGTAACTGTGACATTTGTACTTTGCAATTCATCTTCA 2880  
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QY 2881 TCTTTGCGGTGATGGGAATGCAACTGTTTCGGAAGAATATCATGATCACAAGGACCGCT 2940  
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QY 3061 ATGTCCTGTCATCCCTTCTTCTTGGCCACCGTTGTCATCGGCAATCTTGTGTACTTA 3120  
Db 3121 ACCTTTTCTAGCCTTGTCTTCTTGTCCAAATTTTGGCTCATCTAGCTTATCAGCCGCTG 3180  
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QY 3241 GGTTTAAGCGTATATGCTGATGTTTCAAGTTAATAGCTAACAAATTCACAAATCAAA 3300  
Db 3301 TAAGTATCAACCATCAGGTGAGAGGACCAACAGATCAGTTGATTTGGAGGCAAGAGC 3360  
QY 3301 TAAGTATCAACCATCAGGTGAGAGGACCAACAGATCAGTTGATTTGGAGGCAAGAGC 3360  
Db 3361 ATGGTGACAAACGAACTGGAGCTGGGCCACGACGAGATCTCTCGCCGACGGCTCATCAAGA 3420  
QY 3361 ATGGTGACAAACGAACTGGAGCTGGGCCACGACGAGATCTCTCGCCGACGGCTCATCAAGA 3420  
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QY 3421 AGGGGATCAAGGAGCAGACCAACTGGAGTGGCCATCGGGGATCGGATGGAATTCACGA 3480  
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QY 3481 TACACGGCGACATGAAGAAACAACAAGCCGAAGAAATCCAAATATCTAAATAACGCAACGA 3540  
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QY 3541 TGATTGGCAACTCAATTAACCAACAGACAAATAGACTTGAACACAGACTAAACCATAGAG 3600  
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QY 3661 GACCATTCAGGACGAGAGCCAAAGGCGCAGAGCCGCGAGAGATGGAGGCGGAGGAAGC 3720  
Db 3721 GCACGCCACGACGAGGAGATTTAGTCTCGACGAGGAACCTGGACGAGGAGGCGGAATGCG 3780  
QY 3721 GCACGCCACGACGAGGAGATTTAGTCTCGACGAGGAACCTGGACGAGGAGGCGGAATGCG 3780  
Db 3781 AGGAGGCGCGCTCGAGCGGTGATCATTTATTCATGACACGACGAGGATATCTCGATG 3840  
QY 3781 AGGAGGCGCGCTCGAGCGGTGATCATTTATTCATGACACGACGAGGATATCTCGATG 3840  
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QY 3901 ACATGACTCGCGCTTCTGGCAAGGATGGGCAATTTACGACTGAAACCTTTTCAATTA 3960  
Db 3961 TTGAAAATAAATTTTGAACAGCTGTTATCATCTACTATGATTTTAAAGTAGCTTAGCTT 4020  
QY 3961 TTGAAAATAAATTTTGAACAGCTGTTATCATCTACTATGATTTTAAAGTAGCTTAGCTT 4020  
Db 4021 TGGCATTAGAAGATGTACATCTGCCACAAGACCCACTACTGCAAGGATATTTTACTATA 4080  
QY 4021 TGGCATTAGAAGATGTACATCTGCCACAAGACCCACTACTGCAAGGATATTTTACTATA 4080  
Db 4081 TGGACAGAATATTTAGCGTTATATCTTCTTGGAAATGTTAACTAGTGTGGCGCTG 4140  
QY 4081 TGGACAGAATATTTAGCGTTATATCTTCTTGGAAATGTTAACTAGTGTGGCGCTG 4140  
Db 4141 GCTTCAAGTGTACTTCCACCAACGCGTGGTGTGGCTCGATTTTCGATTTGCTATGCTAT 4200  
QY 4141 GCTTCAAGTGTACTTCCACCAACGCGTGGTGTGGCTCGATTTTCGATTTGCTATGCTAT 4200  
Db 4201 CGCTTATCAACTTCGTTGCTTCACTTGTGGAGCTGGTGTGATTAAGCCCTTCAAGACTA 4260  
QY 4201 CGCTTATCAACTTCGTTGCTTCACTTGTGGAGCTGGTGTGATTAAGCCCTTCAAGACTA 4260





QY 6421 ACTCGGATCGCGAGCATCGTCCGCGACGGCGAGTGCTGAGCCAGGCTCGCCCCC 6480  
Db 6481 CCTCCTAAGATGACGCGAGTATAGCTCTAGA 6513  
QY 6481 CCTCCTAAGATGACGCGAGTATAGCTCTAGA 6513  
RESULT 5  
ID PCT-US95-14262-7 STANDARD; DNA; UNC; 6513 BP.  
AC xxxxxx  
DT Sequence 7, Application PC/TUS9514262  
CC Sequence 7, Application PC/TUS9514262  
CC GENERAL INFORMATION:  
CC APPLICANT: Warmke, Jeffrey W.  
CC APPLICANT: Van Der Ploeg, Leonardus  
CC TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE  
CC TITLE OF INVENTION: PARA SODIUM CHANNEL  
CC NUMBER OF SEQUENCES: 7  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Jack L. Tribble  
CC STREET: P.O. Box 2000, 126 E. Lincoln Avenue  
CC CITY: Rahway  
CC STATE: New Jersey  
CC COUNTRY: USA  
CC ZIP: 07065-0907  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patent In Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: PCT/US95/14262  
CC FILING DATE:  
CC CLASSIFICATION:  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Tribble, Jack L.  
CC REGISTRATION NUMBER: 32,633  
CC REFERENCE/DOCKET NUMBER: 19338 PCT  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (908) 594-5321  
CC TELEFAX: (908) 594-4720  
CC INFORMATION FOR SEQ ID NO: 7:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 6513 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear.  
CC MOLECULE TYPE: cDNA  
CC SEQUENCE 6513 BP; 1681 A; 1548 C; 1702 G; 1582 T; 0 OTHER.  
Query Match 100.0%; Score 6513; DB 2; Length 6513;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 1 TCTAGAGTTGGCGCATAGACAAATGACAGAGATCCGACTCGATATCTGAGGAAGAAC 60  
Db 61 GCAGTTTGTCCGTCCTTTACCGCGGAATCATTTGGTGCAAAATCGAACAACGATTGCCG 120  
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Db 121 CTGAACATGAAAGCAGAGAGCTGGAAAGAGAGAGCCGAGGAGAGTCCCGCAT 180  
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Db 181 ATGGTCCGAAGAAAACAAAAGAAATCCGATATGATGACGAGGACGAGGATGAAGTC 240  
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Db 241 CACAACGGATCCTACACTTGAACAGGGTGTCGCAATACCTGTTTCGATTCGAGGAGCT 300  
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Db 301 TCCCGCCGGAATTTGGCTCCACTCTCTCGAGGATATCGATCCCTACTACACGAATGTAC 360  
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Db 481 CATTTATTTCCCTATTTCATCATCACACAAATTCCTCAACTGCATCCCTGATGATAATGC 540  
QY 481 CATTTATTTCCCTATTTCATCATCACACAAATTCCTCAACTGCATCCCTGATGATAATGC 540  
Db 541 CGACAACGCCACGGTTGAGTCCACTGAGGTGATATTCACCGGAATCTACACATTTGAAT 600  
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QY 601 CAGCTGTTAAAGTGATGGCACGAGGTTTCATTTTATGCCCGTTTACGTTACTTAGAGATG 660  
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QY 661 CATGGAATTTGGCTGGACTTCGTAGTAATAGCTTTAGCTTTATGTGACCATGGGTATAGATT 720  
Db 721 TAGGTAATCTAGACGCCCTGCGAAGCTTTAGGGTGCTGCGAGCGCTTAAACCGTAGCCA 780  
QY 721 TAGGTAATCTAGACGCCCTGCGAAGCTTTAGGGTGCTGCGAGCGCTTAAACCGTAGCCA 780  
Db 781 TTTGTCCAGGCTTGAAGACCATCGTGGCGCGCTCATCGAATCGGTGAAGAAATCTCGCG 840  
QY 781 TTTGTCCAGGCTTGAAGACCATCGTGGCGCGCTCATCGAATCGGTGAAGAAATCTCGCG 840  
Db 841 ATGTGATTTATCTGACCATGTTCTCCCTGCTCGGTGTTCCGTTGATGGCGCTACAGATCT 900  
QY 841 ATGTGATTTATCTGACCATGTTCTCCCTGCTCGGTGTTCCGTTGATGGCGCTACAGATCT 900  
Db 901 ATATGGCGTGTCTACCGGAGAGTGCATCAAGAAGTTCCCGCTGGACGGTTCTCTGGGCA 960  
QY 901 ATATGGCGTGTCTACCGGAGAGTGCATCAAGAAGTTCCCGCTGGACGGTTCTCTGGGCA 960  
Db 961 ATCTGACCCAGCAGAACTCGGGACTATCAAAATCGCAATAGCTCCAAATTTGGTATTCGAGG 1020  
QY 961 ATCTGACCCAGCAGAACTCGGGACTATCAAAATCGCAATAGCTCCAAATTTGGTATTCGAGG 1020  
Db 1021 ACGAGGGCATCTCATTTCCGTTTATGCGGCAATATATCCCGTGGCGGCAATGCGAGGACG 1080  
QY 1021 ACGAGGGCATCTCATTTCCGTTTATGCGGCAATATATCCCGTGGCGGCAATGCGAGGACG 1080  
Db 1081 ATTACGTGTCCCTGACAGGGTTTGGTCCGAATCCGAATTTATGGCTACACAGGTTTCGATT 1140  
QY 1081 ATTACGTGTCCCTGACAGGGTTTGGTCCGAATCCGAATTTATGGCTACACAGGTTTCGATT 1140  
Db 1141 CGTTCGGATGGGTTTCTCTGTCGCGCTTCCGGTGATGACAGAGACTTCTGGGAGATC 1200  
QY 1141 CGTTCGGATGGGTTTCTCTGTCGCGCTTCCGGTGATGACAGAGACTTCTGGGAGATC 1200  
Db 1201 TGTACCAAGTGTGTTGCGCGCGCGGACCATGGCACATGCTGTTCTTTATAGTCATCA 1260  
QY 1201 TGTACCAAGTGTGTTGCGCGCGCGGACCATGGCACATGCTGTTCTTTATAGTCATCA 1260  
Db 1261 TCTTCTTAGGTTCACTTATCTTGTGAATTTGATTTTGGCCATTGTTGCGCATGTCGATG 1320  
QY 1261 TCTTCTTAGGTTCACTTATCTTGTGAATTTGATTTTGGCCATTGTTGCGCATGTCGATG 1320  
Db 1321 ACGAATTCGAAGGAAGCGCCGAAGAGAGGCTGCCGAAGAGGAGCGGATACGTTGAAG 1380  
QY 1321 ACGAATTCGAAGGAAGCGCCGAAGAGAGGCTGCCGAAGAGGAGCGGATACGTTGAAG 1380



Qy	3541	TTGATTGCCAACTCAATTAACCAACCAAGCAATAGACTGGAACAGAGCTAAACCATAGAG	3600
Db	3601	GTTTGTCTTTACAGGACGACGACACTGCCAGCATTAACCTCATATGGTAGCCATAAGAATC	3660
Qy	3601	GTTTGTCTTTACAGGACGACGACACTGCCAGCATTAACCTCATATGGTAGCCATAAGAATC	3660
Db	3661	GACCAATCAAGGACGAGAGCCACAGAGGCGAGCCGAGACGATGGAGGGCGAGAGAAGC	3720
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Qy	3721	GCAGCGCCACGAGGAGGATTTAGTCTCGACGAGAACTGGACGAGGAGGGCGAATGCG	3780
Db	3781	AGGAGGCCCGCTCGACGGTGATATCATTTATTCATGCACAGCAGGAGATATCTCGATG	3840
Qy	3781	AGGAGGCCCGCTCGACGGTGATATCATTTATTCATGCACAGCAGGAGATATCTCGATG	3840
Db	3841	AAATATCCAGCTGATGCTGCCCGGATTCGTACTATAAGAAATTTCCGATCTTAGCCGGT	3900
Qy	3841	AAATATCCAGCTGATGCTGCCCGGATTCGTACTATAAGAAATTTCCGATCTTAGCCGGT	3900
Db	3901	ACGATGACTCGCCGTTCTGGCAAGGATGGGCAATTTACGACTGAAAACITTTCAATTAA	3960
Qy	3901	ACGATGACTCGCCGTTCTGGCAAGGATGGGCAATTTACGACTGAAAACITTTCAATTAA	3960
Db	3961	TTGAAAATAAATATTTTGAACACGCTGTTATCACCTATGATTTTAATGAGTAGCTTAGCTT	4020
Qy	3961	TTGAAAATAAATATTTTGAACACGCTGTTATCACCTATGATTTTAATGAGTAGCTTAGCTT	4020
Db	4021	TGGCATTAGAAGATGATACATCTGCCACAAGACCCATACTGCAGGATATTTTATACTATA	4080
Qy	4021	TGGCATTAGAAGATGATACATCTGCCACAAGACCCATACTGCAGGATATTTTATACTATA	4080
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Qy	4081	TGGACAGAAATTTAGCGTTATATCTTCTTGGAAATGTTAATCAAGTGGTGTGGCGTCG	4140
Db	4141	GCTTCAAAGTGTACTTACCACCGCTGGTGTGGCTCGATTTCTGATGTTCTCATGTGAT	4200
Qy	4141	GCTTCAAAGTGTACTTACCACCGCTGGTGTGGCTCGATTTCTGATGTTCTCATGTGAT	4200
Db	4201	CGCTTATCAACTTCGTTGCTTCACTTTGTSAGCTGGTGGTATTCAGCCCTCAAGACTA	4260
Qy	4201	CGCTTATCAACTTCGTTGCTTCACTTTGTSAGCTGGTGGTATTCAGCCCTCAAGACTA	4260
Db	4261	TGCGAAGCTTTAAGAGCACTGAGACCACTACGTGCCATGTCGCCGATGCAGGGCATGAGG	4320
Qy	4261	TGCGAAGCTTTAAGAGCACTGAGACCACTACGTGCCATGTCGCCGATGCAGGGCATGAGG	4320
Db	4321	TCGTCGTTAATGCGTGGTACAGCTATACCGTCCATCTTCAATGTGCTATTGCTGTGTC	4380
Qy	4321	TCGTCGTTAATGCGTGGTACAGCTATACCGTCCATCTTCAATGTGCTATTGCTGTGTC	4380
Db	4381	TAATATTTTGGCTAAATTTTGCCATAATGGGTGTACAGCTTTTGGTGGAAAAATTTTAA	4440
Qy	4381	TAATATTTTGGCTAAATTTTGCCATAATGGGTGTACAGCTTTTGGTGGAAAAATTTTAA	4440
Db	4441	AGTCGAGGACATGAATGGCAGCAAGCTCAGCCAGAGATCATACCAATCGCAATGCCT	4500
Qy	4441	AGTCGAGGACATGAATGGCAGCAAGCTCAGCCAGAGATCATACCAATCGCAATGCCT	4500
Db	4501	CGGAGCGGAGAACTACAGCTGGTGCATTTACGAAATGAATTCGATCATCTAGTAAACG	4560
Qy	4501	CGGAGCGGAGAACTACAGCTGGTGCATTTACGAAATGAATTCGATCATCTAGTAAACG	4560
Db	4561	CGTATCTGTCCTTTTCCAAAGTGGCCACCTTCAAAGGCTGGATACAAATCATGAACGATG	4620
Qy	4561	CGTATCTGTCCTTTTCCAAAGTGGCCACCTTCAAAGGCTGGATACAAATCATGAACGATG	4620
Db	4621	CTATCGATTCACGAGAGGTGGACAACCAATTCGTGAAACGAACATCTACATGTAAT	4680
Qy	4621	CTATCGATTCACGAGAGGTGGACAACCAATTCGTGAAACGAACATCTACATGTAAT	4680

QY	4621	CTATCGATTTCAGAGAGGTGGACAAAGCAACCAATTCGTGAAACGAACATCTACATGTATT	4680
Db	4681	TATATTTTCGTATTTCTTCATCATATTTGGATCCTTTTTTCACACTCAATCTGTTCATTTGGTG	4740
QY	4681	TATATTTTCGTATTTCTTCATCATATTTGGATCCTTTTTTCACACTCAATCTGTTCATTTGGTG	4740
Db	4741	TTATCATTTGATTAATTTTAAATGAGCAAAAGAAAAGACGAGTGGATCATTTAGAAATGTTCA	4800
QY	4741	TTATCATTTGATTAATTTTAAATGAGCAAAAGAAAAGACGAGTGGATCATTTAGAAATGTTCA	4800
Db	4801	TCGACAGAAGATCAGAAAAAGTACTATAATGCTATGAAABAAGATGGGCTCTAAAAAACCAT	4860
QY	4801	TCGACAGAAGATCAGAAAAAGTACTATAATGCTATGAAABAAGATGGGCTCTAAAAAACCAT	4860
Db	4861	TAAAGGCCATTCCAAGACCAAGGTGGCGACCACAAAGCAATAGTCTTTGAAATAGTAACCG	4920
QY	4861	TAAAGGCCATTCCAAGACCAAGGTGGCGACCACAAAGCAATAGTCTTTGAAATAGTAACCG	4920
Db	4921	ATAAGAAATTCGATATAATCATATTAATGTTATTCATTTGGTCTGAACATGTTCCACCATGACCC	4980
QY	4921	ATAAGAAATTCGATATAATCATATTAATGTTATTCATTTGGTCTGAACATGTTCCACCATGACCC	4980
Db	4981	TCGATCGTTTACGATCGGTTCGGACACGTATAACCGCGTCTAGACTATCTCAATGCGCATAT	5040
QY	4981	TCGATCGTTTACGATCGGTTCGGACACGTATAACCGCGTCTAGACTATCTCAATGCGCATAT	5040
Db	5041	TCGTAGTTATTTTCAGTTCGGAATGTCATTAAAAATATTTCGCTTTACGATATCACTATT	5100
QY	5041	TCGTAGTTATTTTCAGTTCGGAATGTCATTAAAAATATTTCGCTTTACGATATCACTATT	5100
Db	5101	TTATTGAGCCATGGAAATTTATTGATGATAGTGTCTATTATCCATCTTAGGTCCTTG	5160
QY	5101	TTATTGAGCCATGGAAATTTATTGATGATAGTGTCTATTATCCATCTTAGGTCCTTG	5160
Db	5161	TACTTAGCGATATTTCGAGAGAGTACTTCGTGTCGCCGACCCTGCTCCGAGTGGTGGTG	5220
QY	5161	TACTTAGCGATATTTCGAGAGAGTACTTCGTGTCGCCGACCCTGCTCCGAGTGGTGGTG	5220
Db	5221	TGGCGAAAGTGGGCCGTGCTTCGACTGGTGAAGGGAGCGCAAGGGCAATTCGGACACTGC	5280
QY	5221	TGGCGAAAGTGGGCCGTGCTTCGACTGGTGAAGGGAGCGCAAGGGCAATTCGGACACTGC	5280
Db	5281	TCTTCGCGTTGGCCATGTCGCTGCCGGCCCTGTTCAACATCTGCCTGCTCTTCTCTGG	5340
QY	5281	TCTTCGCGTTGGCCATGTCGCTGCCGGCCCTGTTCAACATCTGCCTGCTCTTCTCTGG	5340
Db	5341	TCATGTTTCATCTTTGCCATTTTCGGCATGTGCTTCTTCATGCACTGTAAGGAGCAATCGGACACTGC	5400
QY	5341	TCATGTTTCATCTTTGCCATTTTCGGCATGTGCTTCTTCATGCACTGTAAGGAGCAATCGGAGAGCG	5400
Db	5401	GCATTAACACAGCTCTACAACCTTCAACACCTTTGGCCAGACGATGATCCTGCTCTTTCAGA	5460
QY	5401	GCATTAACACAGCTCTACAACCTTCAACACCTTTGGCCAGACGATGATCCTGCTCTTTCAGA	5460
Db	5461	TGTCGACGTACGCGGTTGGGATGGTGTACTTGGACGCCATTATCAATGAGGAAGCATGCG	5520
QY	5461	TGTCGACGTACGCGGTTGGGATGGTGTACTTGGACGCCATTATCAATGAGGAAGCATGCG	5520
Db	5521	ATCCACCCGACGACGACAAGGCTATCCGGGCAATTTGTGGTTCAGGACCGCGTTGGGAATAA	5580
QY	5521	ATCCACCCGACGACGACAAGGCTATCCGGGCAATTTGTGGTTCAGGACCGCGTTGGGAATAA	5580
Db	5581	CGTTTCTCTCTCATACCTAGTTTATAAGCTTTTGTATAGTTTATATATCTACATGCTG	5640
QY	5581	CGTTTCTCTCTCATACCTAGTTTATAAGCTTTTGTATAGTTTATATATCTACATGCTG	5640
Db	5641	TCATTTCTGAGAACTATAGTCAGGCCACCGAGGACGTGCAAGAGGGTCTTAACCGAGCAGC	5700
QY	5641	TCATTTCTGAGAACTATAGTCAGGCCACCGAGGACGTGCAAGAGGGTCTTAACCGAGCAGC	5700
Db	5701	ACTACGACATGTACTATGAGATCTCGAGCAATTCGATCCGGAGGGGACCCAGTACATAC	5760
QY	5701	ACTACGACATGTACTATGAGATCTCGAGCAATTCGATCCGGAGGGGACCCAGTACATAC	5760





[illegible]



[illegible]

Query Match 0.6%; Score 37; DB 1; Length 5975;  
Best Local Similarity 65.0%;  
Pred. No. 5.73e-08;  
Matches 80; Conservative 0; Mismatches 43; Indels

QY 1 TCTAGACGTTGCCCGCATAGACAATGACAG 30

Search completed: Sun Sep 13 07:25:43 1998  
Job time : 321 secs.



Matches	6513;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Db	1	tctagcgttggcgcgatacacaataacacaaattccgactcgatatctgaggaagac	60						
Qy	1	TTAGAGCTTGGCGGATAGACATGACAGAATTCGGACTCGATATCTGAGGAGAAC	60						
Db	61	gcagttgttcctcccttaccgcggaatcattggtgcaaatcgaaacacgcattgcg	120						
Qy	61	GCAGTTTGTTCGCTCCCTTACCGCGCAATCATTTGGTGTCAATCGAAACACGATTGCCG	120						
Db	121	ctgaacatgaaagcagaagagctggaagaaagagagccgagggagaggttcccgcat	180						
Qy	121	CTGAACATGAAGACAGAGGAGCTGTGAAGAAAGAGAGCCGAGGGAGAGGTCCCGCAT	180						
Db	181	atggtcgaagaaacaaacaaacccggaatccgatatgatgacgagcagagatgaaggtc	240						
Qy	181	ATGTTGTCAGAAACAAACAAAGAAATCCGATATGATGACGAGGACGAGATGAAGTTC	240						
Db	241	cacaacggatctctacacttgaaacaggggtgtgccaatcacctgttctgatttcagggcagct	300						
Qy	241	CACAACGGATCTCTACACTTGAACAGGGTGTGCCAATACCTGTTCGATTGCAGGGCAGCT	300						
Db	301	tccgcgcggaattggcctccactcctcagagatatcgatccctactacagcaattatc	360						
Qy	301	TCCGCGCGGAATTGGCTCCACTCCTCTCGAGGATATCGATCCCTACTACAGCAATGTAC	360						
Db	361	tgacattcgtagttgtaagcaagaaagatatatttccgtttttctgcatcaaaacaa	420						
Qy	361	TGACATTCTGTAGTTGTAAAGCAAGAAAGATATTTTCGCTTTTCTGTCATCAAAACCAA	420						
Db	421	tgtggatgcgtatccattccaatccgatacgtggtgtggtgccaattacattctagtgatc	480						
Qy	421	TGTGGATGCTCGATCCATTCAATCCGATACGTCGTGTGGCCATTACATTCTAGTGCATC	480						
Db	481	cattatttccctattcattccacaaattctcgaactgcactcactcactaataatgc	540						
Qy	481	CATTATTTCCCTATTCTATCATCAACCAATCTCGCACTGCTGCTGCTGCTGCTGCTGCTG	540						
Db	541	cgacaacccacaggttgagtcactgaggtgatattcaccgggaatcacacatttgaat	600						
Qy	541	CGACAACCCACAGGTTGAGTCCACTGAGGTGATATTCACCGGAATCTACACATTTGAAT	600						
Db	601	cagctgttaagtgatggcagaggtttcattttatgcccgtttacgttatcttagagatg	660						
Qy	601	CAGCTGTTTAAAGTATGGCAGCAGGTTTCATTTTATGCCCGCTTACGTTATCTTAGAGATG	660						
Db	661	catggaattggctggaactctgtaaatagcttttagcttatgtaccatgggtatagatt	720						
Qy	661	CATGGAATTGGCTGGACTTCGTAGTAATAGCTTAGCTTATGTGACCATGGGTATAGATT	720						
Db	721	tagtgaattcagcagccctgcgaacgttttaggtgtcgtgcgagcgttaaaaccgtagcca	780						
Qy	721	TAGTGAATCTAGCAGCCCTGCGAACGTTTAGGGTGTCTCGAGCGCTTAAACCCGTAGCCA	780						
Db	781	ttgttccaggttgaagaccatcgtcgcgcgcgtcatcgaaatcgtgaagaatcgcgcg	840						
Qy	781	TTGTTCACAGGTTGAAGACCATCTGTCGCGCGCTCATCGAATCGGTGAAGAATCTGCGCG	840						
Db	841	atgtgattatctgaccattgttctccctgctggtgttgcgttgcgttgcgttgcgttgcgt	900						
Qy	841	ATGTGATTATCTGACCATGTTCCTCTGTGCGGTTCGCGTTGATGGCCCTACAGATCT	900						
Db	901	atatggcggtgtcaccgagagtgatcaagaagtctcccgctggacggttccctggggca	960						
Qy	901	ATATGGCGGTGTCAACCAGAGTGCATCAAGAGTTCCCGCTGCGACGTTCTCTGGGGCA	960						
Db	961	atctaccagcagagactgggactatcaaatcgaatagctccaattggtattccagag	1020						
Qy	961	ATCTACCGACGAGAACTGGGACTATCAATTCGCAATAGCTCCAAATTGGTATTCCCGAGG	1020						
Db	1021	acgagggcatctcatttccgtttatcggaatatatccgggtgcggggcaattgcgacgacg	1080						
Qy	1021	ACGAGGGCATCTCATTTCGTTATCGGCAATATATCCGGTGCGGGGCAATGCGACGACG	1080						

Db	1081	attacgtgtgcctgcaggggtttggtccgaatcccaattatggctacaccaggttcgatt	1140
Qy	1081	ATTACGTGTGCTGCAGGGTITGTTCCGAATCCGAATATGATGCTACACCAGTTCGATT	1140
Db	1141	cgttcggatggccttctcgtccgccttcggcgtgatgacacaggaacttcgggaggtc	1200
Qy	1141	CGTTCGGATGGCTTTCCTGTCCGCTTCCGCTGATACACAGGACTTCTGGGAGGATC	1200
Db	1201	tgtaccagctggtgtgcgcgcgcgacacatgcacatgctgttcttattagtcata	1260
Qy	1201	TGTACAGCTGTGTTCGCGCCGCCGACCATGACATGCTGTCTTATTAGTCATCA	1260
Db	1261	tcttcctaggttcattctcttcttgaattgttttggccattgttgcctatgtcgatg	1320
Qy	1261	TCTTCTAGTTCATTCTATCTTGTGAATTTGATTTGGCCATTGTTGCCATGTCGTATG	1320
Db	1321	acgaattgcaaaaggccggaagaagaagagctgcggaagagagggcgatcacgtgaag	1380
Qy	1321	ACGAATTGCAAAAGGAGCCGGAAGAGAGAGGCTGCCGAAGAGGAGGCGATACGTGAAG	1380
Db	1381	cggaaagaactcgcgcgcgcaaaagcggcgaagctggagagcggcgaatgcagaggtc	1440
Qy	1381	CGGAAGAAGCTGCCGCCCAAGCGGCCAAGCTGGAGGAGCGGCCAATGCGCAGGCTC	1440
Db	1441	aggcagcagcggatgcggctgcgcgcgaagaggtgcactgcacccggaatggtccaaaga	1500
Qy	1441	AGGCAGCAGCGGATGCGCTGCCGGAAGAGAGGCTGCACATCGCAATGCGGAATGCGCAAGA	1500
Db	1501	gtccgacttatcttgcacatcagctatgactattgttgcgcggaagaagcaacgatg	1560
Qy	1501	GTCGACGTTATTTCTTCATCAGCTATGAGCTATTTGTTGGCGCGAAGAGGCAACGATG	1560
Db	1561	acaacaacaaagagaagatgtccattcggagcgtgcgagtgagtgagtcgggtgagcg	1620
Qy	1561	ACAACAACAAAGAGAGATGTCATTTCGGAGCGTCGAGGTGGAGTGGAGTCCGTGAGCG	1620
Db	1621	ttatacaagacaacccagcacctaccacagcacaccaagctaccaaagtctcgtaaagtga	1680
Qy	1621	TTATACAAGACACACAGCACCTTACCACAGCACACCAAGCTACCAAGTTCCTAAAGTGA	1680
Db	1681	gcacgacatccttactcttaccctggttcaccgtttaacatagcaggggatcacgtagtt	1740
Qy	1681	GCACGACATCCTTATCTTACCTGGTTACCGTTTAAACATACGCGGGGATCACGTAGTT	1740
Db	1741	ctacaagttacacga tacggaacggagcgttgcgcgtttggtatacccggtagcgatcga	1800
Qy	1741	CTCACAAGTACACGATACGGAACGGAGCGTGGCGCTTTGGTATACCCGGTAGCGATCGTA	1800
Db	1801	agccattggtattgtcaacatatacagatgccagcagcacttgcctatgcgcgacgt	1860
Qy	1801	AGCCATTGGTATTGTCAACATATCAGGATGCCAGCAGCAGCTTGGCCTATGCGCAGCAGT	1860
Db	1861	cgaatgcgtcaccccgatgtccgaagaagaatggggccatcatagtgcccggttactatg	1920
Qy	1861	CGAATGCCGTACCCCGATGTCCGAAGAGATGCGGCCCATAGTGCCTGTACTATG	1920
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Qy	1921	GCAATCTAGGCTCCCGACACTCATCTATACCTCGCATCAGTCCCGAATATCGTATACCT	1980
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Qy	1981	CAGATGGCGATCTACTCGCGGGCATGGCGCTCATGGCGGTACGACAAATGACCAAGGAGA	2040
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Qy	2041	GCAATGGCCCAACCCCAACACACGCAATCAATCAGTGGSGGCCACCAATGGCGGACCA	2100
Db	2101	cctgtctggacacaaatcacaagctcgatcatcgcgactacgaaattggcctggatgca	2160
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## RESULT 4

ID Q05831 standard; cDNA; 7555 BP.  
AC Q05831;  
DE 10-JAN-1991 (first entry)  
DE Cardiac sodium channel gene.  
KW Rat; arrhythmia; ss.  
OS Rattus rattus.  
PN WO009391-A.  
PF 09-FEB-1990; U00768.  
PR 13-FEB-1989; US-310330.  
PA (ARCH-) ARCH DEV CORP.  
PI Rogart RB.  
DR WPI: 90-275095/36.  
DR P-PSDB: R06584.  
DR New rat cardiac sodium channel proteins - and associated DNA  
PT sequences, polypeptides and peptides associated with  
PT proteins, useful as antiarrhythmic and cardiotoxic drugs.

PS Claim 7; Fig 1; 65pp; English.  
CC The sequence is derived from 3 overlapping clones, pRH3-1, pRH4-23,  
CC and pRH14-31. (Deposited as ATCC 67885, 67886, and 67887 resp.)  
CC The clones were isolated from a cDNA library in the lambda Zap  
CC vector prep. from mRNA obtd. from newborn rat hearts using rat  
CC brain II cDNA probe. The isolated DNA can be used to screen a  
CC similar human derived cardiac cDNA library for the corresponding  
CC human gene. Proteins produced by expression of the DNA have  
CC diagnostic therapeutic, and prognostic applications.  
SQ Sequence 7555 BP; 1576 A; 2314 C; 2101 G; 1564 T;  
Query Match 5.3%; Score 344; DB 1; Length 7555;  
Best Local Similarity 63.3%; Pred. NO. 2,00e-215;  
Matches 1174; Conservative 0; Mismatches 650; Indels 30; Gaps 19;  
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Db 5364 caacacggggctcctactgcagcccaacctgcgcaacgcaacgctcccgccgggggaa 5423
QY 5504 CAAT--GAGGAAGC--A-TGGATCC--ACCCGAC-AGCGACAAAGCTATATCCGGCAA 5554
Db 5424 ctgtggagccgctgggtggcctcctcttccacacattacatcatcctcctcct 5483
QY 5554 TTGTGGTTTACGCGACCGTGTGAATAACGTTCTCTCTCATACCTAGTATTAACGCTTTT 5614
Db 5484 catcgtgtcaacatgtacatgcgcattcctcctcgagacattcagcgtggccgacaggga 5543
QY 5615 GATAGTTATTAATGATGATGCTGTCATTTCTCGAGAACTATAGTCAGGCCACCGAGGA 5674
Db 5544 gagcacagccctgagcggagcagcttcgacatgttcttatgagatctgggagaagtt 5603
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Db 5604 cgaacggagccacacagtcattgattgattctggtccctgcctcctcctcctcctcct 5663
QY 5735 CGATCCGGAGGACCCAGTACATACGCTATGATCAGCTGTGCGCAATTCCTGGACGCTACT 5794
Db 5664 gctcagcgcctccgcatcgcgcaaaccccaacagataagcctcctcaacatggatcctgcc 5723
QY 5795 GGAGCCCGCGTGCAGATCCACAAACCGACAAAGTACAGATCATATCGATGGACATACC 5854
Db 5724 catggtgagcggagacccatcctcctcctcctcctcctcctcctcctcctcctcctcct 5777
QY 5855 CATCTGTGCGCGTACCTCATGTACTGGTGGTGGACATCTCGACGCCCTTAGGAA 5908
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## RESULT 5

```
ID T30192 standard; cDNA; 3033 BP.
AC T30192;
DT 25-OCT-1996 (first entry)
DE Peripheral nervous system sodium channel peptide-1 alpha-subunit gene.
KW Rat; peripheral nervous system; sodium channel; PN1; PC12; PKI-4;
```

```
KW sodium-agonist; sodium-antagonist; drug screening; analgesic;
KW hypertensive; antiinflammatory; trauma; pain; neurological disorder;
KW antisenese; gene therapy; ss.
OS Rattus rattus.
FH Key Location/Qualifiers
FT conflict 1
FT /tag= a
FT /note= "T30193 contains G at this position"
FT 697..1665
FT /tag= b
FT /note= "Probe used in differential tissue
FT expression studies"
FT primer_bind complement (1132..1151)
FT /tag= c
FT primer_bind 1495..1518
FT /tag= d
FT /note= "Binds primer T30196"
FT /note= "Binds primer T30197"
PN W09614077-Al.
PD 17-MAY-1996.
PF 02-NOV-1995; U14251.
PR 02-NOV-1994; US-334029.
PR 07-JUN-1995; US-482401.
PA (TROP-) TROPHIX PHARM INC.
PA (OIN) UNIV NEW YORK STATE RES FOUND.
PI Borden LA, Halegoua S, Mandel G;
DR WPI; 96-251547/25.
DT P-PSDB; R99638.
PT Nucleic acid encoding peripheral nervous system specific sodium
PT channel peptide - useful for sodium channel-associated disease or
PT trauma.
PT Claim 2; Fig 7; 80pp; English.
PS The sequence encodes repeat domain-II of a rat peripheral nervous
CC system sodium channel peptide-1 alpha-subunit (PN1), with sodium
CC channel activity, and has been isolated from a rat PC12 subclone
CC PKI-4 cell culture, expressing high levels of cAMP-dependent
CC protein-kinase-inhibitor. A cDNA library has been screened with
CC primers T30196-97, and the product has been used as a probe to
CC re-screen the library to isolate this sequence. The full-length
CC gene is given in T30193. A probe derived from the sequence may be
CC used in differential tissue expression studies. The peptide may be
CC used to isolate sodium-agonists and sodium-antagonists for use as
CC analgesics, hypotensives, antiinflammatories, and in therapy of
CC sodium channel-associated pathology or trauma, e.g. neurological
CC disorders. The DNA (in sense or antisense orientation) may be used
CC in gene therapy.
SQ Sequence 3033 BP; 860 A; 689 C; 687 G; 797 T;
```

```
Query Match 4.88; Score 312; DB 22; Length 3033;
Best Local Similarity 62.38; Pred. No. 1.22e-192;
Matches 1210; Conservative 0; Mismatches 700; Indels 33; Gaps 21;

Db 736 atgacctgctcagcagtgagctcgtggtttggaagatatctattgaaagaaaaag 795
QY 3996 ATGATTTTAAATGAGTAGCTTTGGCATTTAGAGATGTACATCTGCCACAAGACCC 4055
Db 796 accattaagattatcctcgtgagtgatgctgacaagataatccatcattcctcgtgaa 855
QY 4056 ATACTGCAGGATATTTTATACTATATGGACAGAAATATTTACGGTTATATTTCTTGGAA 4115
Db 856 atgctcttaaatgggtcgcataatgggtataaacatttccactaatcctcgtgttgg 915
QY 4116 ATGTTAATCAAGTGGTGGCGCTCGCGCTTCAAAAGTGTACTTCAACACGGGTGTGG 4175
Db 916 ctggacctcttaattgttgatgctcctcctcctcctcctcctcctcctcctcctcct 915
QY 4176 CTCGATTTCTGATGTGTCATGGTATCGCTTATCAACTTCGTTCTTCTTGGAGCT 4235
Db 976 tcgagaccttggcccccattaaatctctacggacactgagggcccttaagacccttaagacc 1035
QY 4236 GGTGGTATTCAAGCCCTTCAAGACTATGCGAAGCTTAAAGACACTGAGACCACTACGTCGC 4295
Db 1036 ttgctcagatttgaaggaatgagggtagtggtcgaagcactcatagagcaatcccttcc 1095
```



PR 07-JUN-1995; US-482401.  
PA (TROP.) TROPHIX PHARM INC.  
PI Borden LA, UNIV NEW YORK STATE RES FOUND.  
DR WPI; 96-251547/25.  
DR P-PSDB; R99639.  
PT Nucleic acid encoding peripheral nervous system specific sodium  
PT channel peptide - useful for sodium channel-associated disease or  
PT trauma.  
PS Example 1; Fig 9; 80pp; English.  
CC The sequence encodes a rat peripheral nervous system sodium channel  
CC peptide-1 alpha-subunit (PNL) with sodium channel activity, and  
CC has been isolated from a rat PC12 subclone PKI-4 cell culture,  
CC expressing high levels of cAMP-dependent protein-kinase-inhibitor.  
CC A cDNA library has been screened with primers T30196-97, and the  
CC product has been used as a probe to re-screen the library to  
CC isolate the fragment given in T30192. This has been used to isolate  
CC the full-length gene. A probe derived from the sequence may be  
CC used in differential tissue expression studies. The peptide may be  
CC used to isolate sodium-agonists and sodium-antagonists for use as  
CC analgesics, hypotensives, antiinflammatory, and in therapy of  
CC sodium channel-associated pathology or trauma, e.g. neurological  
CC disorders. The DNA (in sense or antisense orientation) may be used  
CC in gene therapy.  
SQ . Sequence 6452 BP; 1816 A; 1454 C; 1550 G; 1632 T;  
Query Match 4.8%; Score 312; DB 22; Length 6452;  
Best Local Similarity 62.3%; Pred. No. 1.22e-192;  
Matches 1210; Conservative 0; Mismatches 700; Indels 33; Gaps 21;  
Db 3920 atgacctcgtcagcagtgaggctcgtggttttgaagatatcttatatgaagaagaaag 3979  
Qy 3996 ATGATTTTAATGAGTAGCTAGCTTGGCATTTAGAAGATGATCATCTGCCACAAAGACCC 4055  
Db 3980 accatgaagtattctcgtgagtagtgcagaaatattcaccatcattcttcattcgaa 4039  
Qy 4056 ATATCGCAGGATATTTATCTATATGACAGATATTTACGGTATATTTCTTTGGA 4115  
Db 4040 atgctctaaatgggtgcgcatgggtataaaacatatctcactaatgcctggtgtgg 4099  
Qy 4116 ATGTTAATCAAGTGGTGGCGCTCGGCTTCAAAGTGTACTTCACCAACGCGTGGTGG 4175  
Db 4100 ctggaactcttaattgttgatgtctcttagtacttagtagcacaactctctggctac 4159  
Qy 4176 CTCGATTTGCGATGTGCATGGTATCGCTTATCAACTTCGTGTCTCACTTTGTTGAGCT 4235  
Db 4160 tcagaccttggcccatataactctcaggaactgaaggccctaaagacccttaagagcc 4219  
Qy 4236 GGTGATTTCAAGCCTTCAAGACTATGCGACGTTAAGAGCAGTACGACACTACGTGCC 4295  
Db 4220 ttgtctagattgaaggaatgaggttagtggtaacgcactcatagagcaatcccttcc 4279  
Qy 4296 ATGCCCCGATGACAGGCGATAGGGGTCGCTTAATGGCTGGTACAAAGCTATACCGTCC 4355  
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Qy 4416 CAGCTTTTGTGGANAATATTTTAAGTCCGAGACATGA---ATGG---CAGCAAGCTCA 4470  
Db 4400 acatcgaattgcaaacccgtctcgtggttttggccctgatgaacgttagtggaaatgtg 4459  
Qy 4471 GC---CAGGAGATCATACCAATTCGAATGCCT-GC---GA-GAGCGAGAAGCT-ACACGTG 4522  
Db 4460 cgatggaaaaacctgaaagtaaaacttcgaaacgttgggtcttggttaccctgtcgtcctt 4519  
Qy 4523 GG-TG---AATTCAGCAA-TGAAATTCGATCATGATGATGAACGCGTATCTGTGCTTTTC 4577  
Db 4520 caagtgcacattcaagggctggtgatgattatgtatgcagcaggttgactctgttaat 4579  
Qy 4578 CAAGTGGCCACTTCARAAGCTGGATACAAATCATGAACGATGCTATCGATTACGAGAG 4637

Db 4580 gtaaatgaacagcgccgaataacgaatacagtcctctacatgtacatttactttgtcatcttc 4639  
Qy 4638 GTGACAAGCAACCAATTCGTGAAACGAACATCTACATGTTATTTATTTTCGTATTCTTC 4697  
Db 4640 atcatctcgtcgtcattctctcactcagttgaacctgttcttctgtcgtcatcatagataatcttc 4699  
Qy 4698 ATCATATTTGGATCTCTTTTTCACACTCAATCTGTTTCATCTGTTGTTATCATTTGATAATTTT 4757  
Db 4700 aaccaacagaa-aaaaaagcttgaggtca--agatatctttatgacagagaacagaag 4756  
Qy 4758 AATGAGCAAAAGAAAAGAGGAGGTGGATCATTTAGAAATGTTTCATGACAGAGATTCAGAAA 4817  
Db 4757 aaatactataatgcaatgaagaagcttggtccaaaaaacacaaacaaatcccaag 4816  
Qy 4818 AAGTACTATTAATGCTATGAAAAGATGGCTCTFAAAAACCATTAAGAAGCCATTCACAGA 4877  
Db 4817 ccagggaacaaatcccaagagtgatatattgacttagtgacaaacaaagcttttgatc 4876  
Qy 4878 CCAAGGTGGGACCCACCAAGCAATAGTCTTTGAAATAGTAACCGATAAGAAATTCGATATA 4937  
Db 4877 accatcgtgttttattatgctcacaatggttaacctgatggttagaaaaagaggggcaa 4936  
Qy 4938 ATCATTTATGTTTCAATTGCTGTAACATGTTCAACATGACCCCTCGATCGTTACGATCGC 4997  
Db 4937 actgagtacatggattatgtttacactggtcaacatggtcttcattcttacttcttccact 4996  
Qy 4998 TCGGACAGCTATACGCGGTCTTAGACTATCTCAATCGGATATTCGTAGTTATTTTCAGT 5057  
Db 4997 ggggagtgctgctggaagctaatctccctcagacattactacttctcactgtgggttggaac 5056  
Qy 5058 TCCGAATGTCTATTAAAAATATTTCGCTTTACGATATCACATATTTTATTGAGCCATGGAAT 5117  
Db 5057 attttgatatttggtagtactctcactcactcactcactcactcactcactcactcactcactcact 5116  
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Qy 5178 GAGAAGTACTTCGTGTGCGCGACCCCTCTCGAGTGGTGGTGGGGAAGTGGGCGGT 5237  
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Qy 5238 GTCTTCAGCTGTGTGAAGGAGGCAAGGCAATTCGGACACTGTCTCTCGGCTTGGCCAT 5297  
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Qy 5298 TCGGTGCGGCGCCCTGTTCACATCTGCCTGCTGCTGTCTCTGTTCTGTTCTGTTCTGTTCTG 5357  
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Db 5477 gttcacccaggaagtgctcagtggaaggggactgtgggaacccatccctgggggattttttac 5536  
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Db 5537 ttgtcagctacatcatcatcttctcgttgggtgggtggaacatgtacatcgtcgtc 5596  
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QY 4543 TCGATCATGTAGGTAACCGGTATCTGTGCCCTTTTCCAAAGTGGCCACCTTCAAAAGCCTGGA 4602
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Db 5290 ttctcgtggttggtgaaacatgatatactgcagtcatactggaagaatttttagtggctccact 5349
QY 5610 TTTTGTAGTATTAAATATGATACATGCTGTCATCTTCTCGAAGAACTATAGTCAGGCCACC 5669
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Db 5350 gaagaaagtactgaacctctagtgaggatgactttbgagatgttctatgatgaggtttggag 5409
QY 5670 GAGGACGTGCAAGAGGTCTTAACCGACGACGACTACGACATGTACTATGAGATCTGSCAG 5729
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## RESULT 9

ID T77803 standard; cDNA; 6524 BP.

AC T77803;

DT 09-OCT-1997 (first entry)

DE cDNA encoding wild type rat DRG (SNS-B).

KW Rat; sensory neuron sodium channel protein; insensitive; tetrodotoxin;

KW modulator; impulse; sensory neuron; acute pain; chronic pain;

KW neuropathic pain; glia; muscle; parasympathetic nervous system;

KW enteric nervous system; central nervous system; dorsal root ganglia;

KW cranial ganglia; ss.

OS Rattus rattus.

PH Key Location/Qualifiers

FT cds 204..6077

FT /\*tag= a

FT /product= Rat\_DRG (SNS-B)

PN WO9701577-A1.

PD 16-JAN-1997; G01523.

PF 25-JUN-1996; G01523.

PR 28-JUN-1995; GB-013180.

PA (UNLO ) UNIV COLLEGE LONDON.

PI Akopian AN, Wood JN;

DR WPI; 97-100165/09.

DR P-PSDB; W21737.

PT New isolated mammalian sensory neuron sodium channel protein - used

PT to identify modulators of the sodium channel, partic. for the

PT treatment of pain

PS Claim 9; Page 50-58; 128pp; English.

CC The sequences given in T77803-06 encode the wild type and three

CC variant forms of a rat sensory neuron sodium channel protein which

CC is insensitive to tetrodotoxin. The proteins can be used for

CC identifying modulators of the sodium channel. Blockers of the

CC sodium channel will block or prevent the transmission of impulses

CC along sensory neurons and thereby be useful in the treatment of acute,

CC chronic or neuropathic pain. The novel protein is found only in sensory

CC neurons and not in glia, muscle or the neurons of the (para)sympathetic,

CC enteric or central nervous system. The protein is found preferably in

CC the neurons of the dorsal root ganglia or cranial ganglia.

SQ Sequence 6524 BP; 1540 A; 1866 C; 1662 G; 1456 T;

Query Match 4.5%; Score 296; DB 32; Length 6524;

Best Local Similarity 63.8%; Pred. No. 2.83e-181;

Matches 890; Conservative 0; Mismatches 486; Indels 18; Gaps 11;

Db 4254 aacttcgacacgtcgctatggcctacctgcactcttcaggtggcaaccttcaaggc 4313

QY 4539 AATTCGATCATGTAGTAAACGCGTATCTGCTTTTCCAAAGTGGCACCTTCAAGGC 4598

Db 4314 tggatgacataatgtatgcagctgttgatcccgagagatcaacagtcagcctaactgg 4373

QY 4599 TGGATAAAATCATGAACGATGCTATCGATTTCACGAGAGGTGGACAAGCAACCAATTCGT 4658

Db 4374 gagaacaactgtacatgtaccctgactctgttgcttcttcacatcttctcgttgcttc 4433

QY 4659 GAAACGAACATCTACATGTATTTATATTTCTTCTTCATCATATTGATGCTCTTTTC 4718















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```
Run on:      Sun Sep 13 04:30:04 1998; MasPar time 6599.57 Seconds
           1382.167 Million cell updates/sec
Tabular output not generated.
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Scoring table: TABLE default

Searched: 1832099 seqs, 700269816 bases x 2

Database: emb1-est55

Statistics: Mean 12.798; Variance 2.257; scale 5.669

## SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description	Pred. No.
		Match	%					
1	124	1.9		343	21	HSC2HD061	H. sapiens partial cDN	1.16e-19
2	121	1.9		529	24	AA183990	m53E02.r1 Life Tech m	4.89e-19
3	99	1.5	594	25	AA272867	vb9f10.r1 Soares mous	4.27e-14	
4	91	1.4	619	26	FR0002753	F.rubripes GSS sequenc	5.18e-12	
5	77	1.2	413	10	AA427267	ve83f11.r1 Soares mous	1.01e-97	
C	-76	1.2		706	18	AA984063	am76509.s1 Stratagene	1.15e-95
C	7	70	1.1	252	13	AA754459	ES7N1787 Rice Immature	1.93e-83
C	8	62	1.0	214	4	RA360938	EGT70140 T-cell Lympho	1.68e-67
9	64	1.0	252	13	AA754459	ES7N1787 Rice Immature	1.92e-71	
10	67	1.0	328	16	AA914778	v209a09.r1 Stratagene	2.07e-77	
11	65	1.0	573	11	AA692527	HL08049.5Prime HL Dros	2.00e-73	
12	59	0.9	242	3	AA754458	97SN1784 Rice Immature	1.19e-61	
13	60	0.9	247	13	AA754458	97SN1784 Rice Immature	1.36e-63	



**JOURNAL  
COMMENT**

Unpublished (1996)

Contact: Marra M/Mouse EST Project  
WASHU-HHMI Mouse EST Project  
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Tel: 314 286 1800  
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Email: [mouseest@watson.wustl.edu](mailto:mouseest@watson.wustl.edu)  
 This clone is available royalty-free through LLNL ; contact the  
 IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.

MGI:457443  
Seq primer: -28ml3 rev2 ET from Amersham  
High quality sequence stop: 456.

FEATURES	SOURCE
1. <b>High Accuracy:</b> The model achieves a high accuracy rate, indicating its effectiveness in predicting the target variable.	Model Performance Metrics
2. <b>Robustness:</b> The model demonstrates robustness against various input variations and noise, ensuring reliable predictions.	Model Performance Metrics
3. <b>Interpretability:</b> The model's predictions are interpretable, allowing users to understand the underlying factors influencing the outcome.	Model Performance Metrics
4. <b>Scalability:</b> The model is scalable, capable of handling large volumes of data and complex tasks efficiently.	Model Performance Metrics
5. <b>Real-time Processing:</b> The model supports real-time data processing, enabling immediate insights and decision-making.	Model Performance Metrics
6. <b>Integration with Existing Systems:</b> The model seamlessly integrates with existing data systems and workflows, facilitating easy adoption.	Model Performance Metrics
7. <b>Customizable Parameters:</b> The model offers customizable parameters, allowing users to tailor the model to specific requirements.	Model Performance Metrics
8. <b>Comprehensive Documentation:</b> The model is accompanied by comprehensive documentation, providing detailed information on its usage and capabilities.	Model Performance Metrics
9. <b>Regular Updates:</b> The model is regularly updated with the latest data and algorithms, ensuring its performance remains state-of-the-art.	Model Performance Metrics
10. <b>Support and Training:</b> The model is supported by a dedicated team, offering training and assistance to users.	Model Performance Metrics

```

1..594
/organism="Mus musculus"
/vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TCTTACCAATCGAGTCGGACGCCGCGAATCTTTTTTTTTTTT 3'];
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
constructed and normalized by Bento Soares and M.Fátima
Bonaldo."
/db_xref="taxon:10090"
/clone="748459"
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98	98	98
99	99	99
100	100	100

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ch      1.5%; Score 99; DB 25; Length 594;
l Similarity 73.0%; Pred.No. 4.27e-144;
157; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

```

ATCCCAACTACGGCTACACCAGCTTCGACACCTTCAGCTGGGCCCTCCTGGCACGGTTC 224  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
TCCGAATTATGGCTACACCAGCTTCGATTCTGTTCGGATGGGCCTTCCTGTCCGCCCTC 1169

GCCTCATGACTCAGGACTACTGGGAGAACTTATACCAGCTGACCTACGAGCGGCTGGG 284

GGCTGATGACACAGGACTTCTGGGAGGATCTGTACCAGCTGGTGTGCGCGCCGCCGGA 1229  
AAAGTACATGATCTTCTTTGTCTTGGTGATCTTCGCGGTTCTTTCTATTGGTGAAC 344

ATATGGCAGCATGCTGTTCTTTATAGTCATCATCTTCTTAGGTTCAATCTATCTTGTGAAT 1289  
TGCATCTTGGCTCTGGTGGCCATGGCTTACGAACA 1370

TGATCTTGGCTGGTGGCCCATGGCTTACGAAGA 379  
 ||| ||||| ||| ||||| ||| ||| |||  
 TGATTTTGGCCATTGTTGCCATGCGTATGACGA 1324

FR0002753	619 bp	DNA	GSS	27-FEB-1997
-----------	--------	-----	-----	-------------

F.rubripes GSS sequence, clone 010M03aE5, genomic survey sequence  
Z86536  
g1883448

GSS; genome survey sequence.  
Fugu rubripes.  
Fugu rubripes  
Fugu rubripes

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Eugu-

1 (bases 1 to 619)  
Elgar, G., Clark, M., Smith, S., Meek, S., Warner, S., Umrana, Y.,  
Williams, G. and Brenner, S.

Submitted (18-FEB-1997) MRC Human Genome Mapping Project Resource

**COMMENT**

Centre Hinxton, Cambridge, CB10 1SB. Email: [biohelp@hgmpr.mrc.ac.uk](mailto:biohelp@hgmpr.mrc.ac.uk)  
 Vector: ml3mpl8  
 V\_type: phage  
 PRIMER: M13  
 DESCR:

DESCR:  
One pass dye-terminator sequencing of cosmid cloned genomic sequence.

## FEATURES

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Location/Qualifiers
1. .619
/organism="Fugu rubripes"
/db_xref="taxon:31033"
/clone_lib="cosmid 010M03"
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BASE COUNT	156 a	164 c	177 g	120 t	2 others
ORIGIN					

Query Match	1.4%	Score 91;	DB 26;	Length 619;
Best Local Similarity	65.0%	Pred. No. 5.18e-127;		
Matches	195;	Conservative	0;	Mismatches 105;
				Indels
				0;
				Gaps
				0;
Db	17	CTTCTCTATCGTGGTCCAACTNTACATGCCATCCATCCCTGGAGAACTTCAGTGTGCCAC	76	
QY	5609	CTTTTGTATAGTTATTAAATGATACATTGCTGTCATTCTCGAGAACTATAGTCAGGCCAC	5668	
Db	77	GGAGGAGAGCAGCGGCCCTGAGCGAGGATGACTTTGAAATGTTCTATGAGGTTTGGGA	136	
QY	5669	CGAGGAGCTCAAGAGGGTCTACCCGACGAGCTACGACATGTAATGAGATCTGGCA	5728	
Db	137	GAGTTTCGACCCAGAGCCACACAGTTTCATCGAGTAGTACGCCAAGTTGTCGAGACTTTGCAGA	196	
QY	5729	GCAATTCGATTCGAGGGGACCCAGATACATACGCTATGATCAGCTGCGAAATCCTCGA	5788	

QY	3729	GC	AAATTCGATCCGGAGGGGACCCAGATACATAGGCTATGATCAGCTGTCCCGGAATTCCTGGA	3788
Db	197	CT	CTCTCTCAGAACCACTCGGGATCGCCACCACTTAAACAAGATCAAGCTGATCTCCCATGGA	256
QY	5789	CG	TACTGGAGCCCCGCTGCAGATCCCAACAACCGACAAGTACAAGATCATATCGATGGA	5848
Db	257	TC	TGCCGATGTGTACGGGGGACAAATCCATCGCTCGATATCTCTTTTGGCTTTCACAA	316
QY	5849	CAT	ACCATCTGTTCGGGTGACCTCATGTACTGGGTGGACATCTCTGACGCCCTTACGAA	5908

## RESULT

LOCUS	AA427267	413 bp	EST	16-OCT-1997
DEFINITION	ve83f11.r1 Soares mouse NbMh Mus musculus cDNA clone 832845 5' similar to gb:M94055 SODIUM CHANNEL PROTEIN, BRAIN II ALPHA SUBUNIT (HUMAN); gb:U26707 Mus musculus voltage-gated sodium channel alpha subunit SCN8A (MOUSE);, mRNA sequence.			

ACCESSION  
NID

KEYWORDS	EST.	house mouse.	Mus musculus
SOURCE			
ORGANISM			

ORGANISM      MUS MUSCULUS  
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS  
1 (bases 1 to 413)  
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Stepcio, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Willson, R. and Waterston, R.

**TITLE** The WashU-HHMI Mouse EST Project  
**JOURNAL** Unpublished (1996)

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WashU-HHMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501  
Tel: 314 286 1800  
Fax: 314 286 1810

Fax: 314 200 1010  
 Email: mouseest@watson.wustl.edu  
 This clone is available royalty-free through LLNL ; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:493061





Contact: Eun M. Y.  
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Suwon, Kyunggido, Korea  
Tel: 82 331 290 0301  
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Email: myeungsun20.asti.re.kr  
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji  
University, Yongin, Korea. 449-728 bhnaahm@bioserver.myongji.ac.kr  
Seq primer: M13 Reverse Primer.

```

FEATURES
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      1. .252
        /organism="Oryza sativa"
        /cultivar="Milyang23"
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XhoI; Directional cDNA library inserted into lambda ZAPII
vector at 5' end with EcoRI and 3' end with Xho I site."
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        /clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library"
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        /lab_host="E. coli SOLR"
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BASE COUNT
ORIGIN

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[illegible]

RESULT	8	AA360938	214 bp	mRNA	EST	21-APR-1997
LOCUS		EST70140	T-cell lymphoma	Homo sapiens	cDNA 5'	end similar to
DEFINITION			similar to sodium channel 1,	mRNA sequence.		
ACCESSION		AA360938				
NID		NID				
KEYWORDS		G2013258				
SOURCE		EST.				
ORGANISM		human.				
		Homo sapiens				
		Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;				
		Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae;				
		Homo.				

REFERENCE  
AUTHORS

1. (bases 1 to 214)

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Well, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dmke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,

Kozak, D. L., Kunsch, C., Hungjun, J., Li, H., Meisner, P. S., Olsen, H., Raymond, L., Wei, Y. F., Wing, J., Xu, C., Yu, G. T., Ruben, S. M., Dillion, P. J., Fannon, M. R., Rosen, C. A., Haseltine, W. A., Fields, C., Fraser, C. M., and Venter, J. C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

Nature 377 (6547 Suppl), 3-174 (1995)

96036280

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The Institute for Genomic Research  
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Tel: 3018699036

Fax: 3018059423  
 Email: arkerlav@tigr.org  
 For clone availability, additional sequence and expression  
 information related to this EST, please check the TIGR Human Gene  
 Index (<http://www.tigr.org/tldb/hgi/hgi.html>)  
 Seq primer: M13 Reverse.

FEATURES  
SOURCE

```

Location/Qualifiers
1. .214
/organism="Homo sapiens"
/note="vector: pBluescript SK-; Site_1: EcoI"
XhoI"

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Query Match 1.0%; Score 62; DB 4; Length 214;  
Best Local Similarity 75.4%; Pred. No. 1.68e-67;  
Matches 95; Conservative 0; Mismatches 30; Indels

D <sub>b</sub>	89	AAGTTNGACATCCCAAGAATGGCATAGATAAACAATGCCAGGAAGCAGGAGCGCGATG	148
C <sub>p</sub>	5377	AAGAACACATGCCGRAAAATGGCAAAGATGAACATGACCAGGAACAGCACGAGGCAGATG	5318
D <sub>b</sub>	149	TTAACAACGCGAGGAGGGACATCATCAANNCAAAGCAGCAGCTTTCGGATCCCCCTTG C	208
C <sub>p</sub>	5317	TTGAACAGGGCGGCGACGACATGGCCAACGCCAAGACAGAGTGTCT-CGAATTGCCCTTGGC	5259
D <sub>b</sub>	209	TCCTTT	214
C <sub>p</sub>	5258	TCCTTT	5253

RESULT	9
LOCUS	AA754459 252 bp mRNA EST 20-JAN-1998
DEFINITION	Oryza sativa cDNA clone 97SN1787, mRNA sequence.

ACCESSION	AA/34433
NID	92801165
KEYWORDS	EST.
SOURCE	rice.
ORGANISM	Oryza sativa

ORGANISM  
*Oryza sativa*  
Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;  
Embryophyta; Tracheophyta; seed plants; Magnoliophyta; L  
Poales; Poaceae; Oryza.

REFERENCE  
AUTHORS  
1 (bases 1 to 252)  
Nahm, B. H., Kim, J. K., Cheong, J. J., Kim, S. I., Hahn, T. R., Moon, E. P.,  
Kim, W. T., Kim, W. Y., Yang, M. S., Park, R. D., Sohn, U. I., Kang, K. Y.,  
Lee, M. C. and Eun, M. Y.  
Large-scale Sequencing Analysis of ESTs from Rice Immature Seed  
Unpublished (1998)  
JOURNAL

Contact: Eun M.Y.  
Department of Cytogenetics  
National Inst. of Agri. Sci. and Tech, RDA  
Suwon, Kyunggido, Korea





[illegible]

Search completed: Sun Sep 13 07:01:11 1998  
Job time : 9067 secs.

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